RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
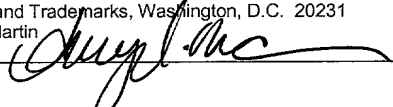
APPLICATION FOR UNITED STATES
LETTERS PATENT

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Description

RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME

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Cross Reference to Related Applications

This application is based on and claims priority to United States Provisional Application Serial Number 60/235,654, filed September 26, 2000, herein incorporated by reference in its entirety.

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Grant Statement

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Technical Field

The present invention relates generally to compositions and methods for identifying oligonucleotide sequences that specifically bind biomolecules, including peptides, hydrophobic molecules, and target features on cell

20 surfaces, in particular extracellular proteins, and the use of these sequences to detect and/or isolate the target molecules and the resulting compositions. The instant invention is exemplified by obtaining compositions, through the use of disclosed methods, that comprise oligonucleotide sequences that bind to coagulation factors, E2F family transcription factors, Ang1, Ang2, and

25 fragments or peptides thereof. Even more particularly, the present invention is directed towards ribonucleic acid (RNA) aptamers, and to methods of identifying them.

Table of Abbreviations

30   I - XII   coagulation factors

a	activated, as in factor VIIa, IXa, Xa, etc.
ACT	activated clotting time
Ang1	Angiopoietin-1
Ang1*	activated Angiopoietin-1
Ang2	Angiopoietin-2
Ang2*	activated Angiopoietin-2
aPTT	Activated Partial Thromboplastin Time
DNA	deoxyribonucleic acid
DP	diphosphate
FB	fraction bound
GTP	guanidine triphosphate
K_d	dissociation constant
M7G	5-adenosyl-L-methonine substituted GTP
MP	monophosphate
nM	nanomolar
PAC	phenoxyacetyl
pM	picomolar
PT	Prothrombin Time
RNA	ribonucleic acid
SELEX	Systematic Evolution of Ligands by EXponential Enrichment
sem	standard error for mean
TAC	t-butoxyacetyl
TOG	toggle
TP	triphosphate

Background Art

Thrombin belongs to the group of serine proteases and plays a central part in the blood coagulation cascade as terminal enzyme. Both the intrinsic and the extrinsic coagulation cascade lead, via a plurality of amplifying stages, to the production of thrombin from prothrombin. Thrombin-catalyzed cleavage of fibrinogen to fibrin then initiates blood coagulation and aggregation of platelets that, in turn, due to the binding of platelet factor 3 and

coagulation factor XIII and a large number of highly active mediators, enhance thrombin formation.

To elaborate, the mechanism of blood coagulation normally occurs in a cascade of two possible routes. One of the routes, the extrinsic blood coagulation, starts with the liberation of thromboplastin and the activation of factor VII. Activated factor VII (i.e. factor VIIa) in turn activates factor X, followed by an activation of factor V and factor II (prothrombin). Factor IIa (thrombin) converts fibrinogen into fibrin at the end of the cascade.

The other route, the intrinsic blood coagulation, occurs via an activation of factor XII by contact with and subsequent activation of factor XI, factor IX and factor X in the presence of calcium and factor VIII, followed by an activation of thrombin (factor II) to activated thrombin (factor IIa) which triggers coagulation by cleaving fibrinogen to fibrin. Thus, activated thrombin (factor IIa) plays a role in both routes of the blood coagulation cascade.

Hitherto, there has been an intensive search for anticoagulants that can particularly be utilized in the treatment of cardiovascular disease, e g. septic shock, thromboses, embolisms, atherosclerosis and cardiac infarctions, furthermore in case of blood transfusions or following surgery. One method of suppressing the coagulation of blood is the direct administration of substances that modulate thrombin or other coagulation factors. The identification of such substances thus represents a long-felt and ongoing need in the art.

E2F refers to a family of transcription factors (also referred to herein as the "E2F family", which includes but is not limited to E2F-1, E2F-2, E2F-3, E2-F4, E2-F5 and E2-F6), and E2F activity is plays a role in a wide variety of proliferative events. E2F activity is controlled as the end result of G_1 cyclin dependent kinase regulatory cascades that involve the Rb family of proteins. See, e.g., Sherr, C.J., *Cell*, 73:1059-1065 (1993); Hunter, T., *Cell* 75:839-841 (1993); Nevins J.R., *Science*, 258:424-429 (1992); Helin, K. and Harlow, E., *Trends Cell Biol.* 3:43-46 (1993); La Thangue, N.B., *Trends Biochem. Sci.* 19:180-114 (1994); Sherr, C.J.; Roberts, J.M., *Genes Dev.* 9:1149-1143 (1995); Weinberg, R.A. *Cell* 81:323-330 (1995); Harbour, J.W. and Dean, D.C., *Genes and Development* 14:2393-2409 (2000); and Black, A.R. and Azizkhan-Clifford, J., *Gene* 237:281-302 (1999). Thus, ligands that selectively

bind to an E2F family member would play a role in the control of cell proliferation, which is of central importance to the proper development of a multi-cellular organism, the homeostatic maintenance of tissues, and the ability of certain cell types to respond appropriately to environmental cues.

5   Tie2 is an endothelial receptor tyrosine kinase (RTK) that is required for both embryonic vascular development and pathological angiogenesis. Tie2 is unique among RTKs in that it has two ligands with apparently opposing actions. Angiopoietin-1 (Ang1) is an activating ligand while Angiopoietin-2 (Ang2) is thought to be a naturally occurring antagonist for

10   Tie2. Mice lacking Tie2 or Ang1 die midway through gestation due to abnormalities of vascular morphogenesis characterized by deficient recruitment of supporting smooth muscle cells and pericytes. Moreover, Ang1 promotes endothelial cell survival and blocks the increases in vascular permeability induced by vascular endothelial growth factor (VEGF), supporting

15   a role for Ang1 in the stabilization and maintenance of the adult vasculature. In contrast, Ang2 is required for VEGF-mediated angiogenesis, and in the absence of endothelial mitogens Ang2 may induce vascular regression.

The exact mechanism of action of the Angiopoietins remains to be elucidated. For example, high-dose Ang2 can induce downstream activation

20   of Akt and endothelial cell survival, suggesting that it does not simply exert a dominant negative effect on Tie2. The need for improved understanding of these ligands' function is particularly important in the study of tumor angiogenesis, as several studies have now shown that inhibition of Tie2 with a soluble receptor blocks tumor growth, angiogenesis, and metastasis.

25   However, it is unclear whether these effects are due to inhibition of the effects of Ang1 or Ang2, since a soluble receptor would bind both ligands. Specific inhibitors of these ligands have the potential to more precisely modulate Tie2 signaling and serve as valuable therapeutic agents.

Aptamers can comprise single-stranded or double-stranded nucleic

30   acids that are capable of binding proteins or other small molecules. Aptamers that have therapeutic value would most likely bind proteins involved in regulatory cascades. The presence of the aptamer would act as a sink for the protein factors, preventing the factors from carrying out their normal functions. To date, only a few aptamers are known.

It would be desirable to identify novel aptamers that bind to factors in the coagulation cascade, to an E2F family member, or to an angiogenesis factor. Indeed, among other applications, such aptamers have utility in the modulation of coagulation, cell proliferation or angiogenesis, and would thus

5   meet a long-felt and continuing need in the art.

Summary of the Invention

An RNA aptamer that selectively binds a coagulation pathway factor, that selectively binds an E2F family member, or that selectively binds an

10   angiogenesis factor (e.g. Ang1 and/or Ang2) is provided in accordance with the present invention. Preferably, the binding affinity for the RNA aptamer for the coagulation pathway factor is represented by a dissociation constant of about 20 nanomolar (nM) or less. Optionally, the coagulation pathway factor is selected from the group consisting of thrombin, activated thrombin, IXa, X,

15   Xa, VII, VIIa and combinations thereof. Most preferably, the RNA aptamers selectively bind activated coagulation factors.

A method of modulating the biological activity of a coagulation pathway factor is also provided in accordance with the present invention. The method comprises: (a) administering to a warm-blooded vertebrate in need thereof an

20   effective amount of an RNA aptamer that selectively binds a coagulation pathway factor, the RNA aptamer having a dissociation constant for the coagulation pathway factor of about 20 nM or less; and (b) modulating the biological activity of the coagulation pathway factor in the warm-blooded vertebrate through the administering of the RNA aptamer in step (a).

25   A method of treating cardiovascular disease in a warm-blooded vertebrate is also provided in accordance with the present invention. The method comprises administering an effective amount of an RNA aptamer that selectively binds a coagulation pathway factor, the RNA aptamer having a dissociation constant for the coagulation pathway factor of about 20 nM or

30   less, to a vertebrate subject suffering from cardiovascular disease, whereby cardiovascular disease in the vertebrate subject is treated.

A method of modulating E2F activity in a warm-blooded vertebrate in which said modulation is desired is also provided. The method comprises: (a) administering to the warm-blooded vertebrate an effective amount of an

RNA aptamer that selectively binds an E2F family member, the RNA aptamer having a dissociation constant for the E2F family member of about 20 nM or less; and (b) modulating E2F in the warm-blooded vertebrate through the administering of the RNA aptamer of step (a).

A method of modulating Ang1 or Ang2 activity in a warm-blooded vertebrate in which said modulation is desired is also provided. The method comprises: (a) administering to the warm-blooded vertebrate an effective amount of an RNA aptamer that selectively binds Ang1 or Ang2, the RNA aptamer having a dissociation constant for Ang1 or Ang2 of about 20 nM or less; and (b) modulating Ang1 or Ang2 in the warm-blooded vertebrate through the administering of the RNA aptamer of step (a).

A method of identifying a ligand to a target from a candidate mixture of potential ligands is also provided in accordance with the present invention. Products, i.e., ligands, produced or identified via the method are also provided in accordance with the present invention.

In a preferred embodiment the method comprises: (a) preparing a candidate mixture of potential ligands; (b) contacting the candidate mixture with a target in a lower stringency buffer, wherein ligands having increased affinity to the target relative to the candidate mixture bind to the target; (c) removing unbound candidate mixture; and (d) collecting the ligands that are bound to the target to produce a first collected ligand mixture. More preferably, the method further comprises: (e) contacting the first collected ligand mixture with the target in a higher stringency buffer, wherein ligands having increased affinity to the target relative to the first collected ligand mixture bind to the target; (f) removing unbound ligands; and (g) collecting the ligands that are bound to the target to produce a second collected ligand mixture to thereby identify ligands to the target. Even more preferably, ligands in the first or second collected ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the first collected ligand mixture with the target in the higher stringency buffer, after collecting the ligands that bound the target in the higher stringency buffer, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce a desired ligand. Thus, it is possible that the second collected ligand mixture can comprise a single ligand.

Another embodiment of a method of identifying a ligand to a target from a candidate mixture of potential ligands is provided in accordance with the present invention. Products, i.e., ligands, produced or identified via the method are also provided in accordance with the present invention.

5   The method preferably comprises: (a) providing a target selected from a first species of organism; (b) preparing a candidate mixture of potential ligands; (c) contacting the candidate mixture with the target, wherein ligands having increased affinity to the target from the first species of organism relative to the candidate mixture bind to the target from the first species of 10   organism; (d) removing unbound candidate mixture; (e) collecting the ligands that are bound to the target from the first species of organism to produce a first collected ligand mixture for the target; (f) contacting the first collected ligand mixture with a target from a second species of organism, the target from the second species having at least a portion thereof that is substantially 15   homologous to the same portion in the target from the first species, wherein ligands having increased affinity to the target from the second species relative to the first collected ligand mixture bind to the target; (g) removing unbound first collected ligand mixture; and (h) collecting the ligands that are bound to the target from the second species of organism to form a second collected 20   ligand mixture thereby identify ligands to the target.

Preferably, ligands in the first or second collected ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the first collected ligand mixture with the target from the second species of organism, after collecting the ligands that bound the target from the 25   second species of organism, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce a desired ligand. Thus, it is possible that the second collected ligand mixture can comprise a single ligand.

It is therefore an object of the present invention to provide novel RNA 30   aptamers that selectively bind coagulation factors, an E2F family member, Ang1 or Ang2. The object is achieved in whole or in part by the present invention.

An object of the invention having been stated hereinabove, other objects will become evident as the description proceeds, when taken in

connection with the accompanying Figures and Laboratory Examples as best described herein below.

Brief Description of the Drawings

5 Figure 1A depicts sequences (SEQ ID NOs:1-12) of representative RNA aptamers of the present invention that bind to and inhibit the activity of coagulation factor IXa.

Figure 1B depicts sequences (SEQ ID NOs:13-22) of representative RNA aptamers of the present invention that bind to and inhibit the activity of
10 coagulation factor IXa.

Figure 2A is a plot of data points showing that RNA 9.3 (SEQ ID NO:3) inhibits the FIXa/FVIIIa catalyzed activation of FX, thereby demonstrating that RNA 9.3 (SEQ ID NO:3) inhibits the activity of coagulation factor IXa. Factor IXa (0.5 nM) was equilibrated with no RNA (▲), 10 nM control RNA (■), or 10
15 nM RNA 9.3 (SEQ ID NO:3) (●), the FX activation reaction was initiated by the addition of FVIIIa (1 nM), PC/PS vesicles (100 μM) and FX (200 nM), and the amount of FXa formed over time at 37°C was measured.

Figure 2B is a bar graph showing that RNA 9.3 (SEQ ID NO:3) prolongs the clotting time of human plasma, thereby demonstrating RNA 9.3
20 (SEQ ID NO:3) inhibits the activity of coagulation factor IXa. The clotting time of normal human plasma was measured in an aPTT assay in the absence of RNA (striped bar), or in the presence of increasing concentrations of control RNA (solid bar) or RNA 9.3 (SEQ ID NO:3) (open bar). The clotting time is expressed as the mean ± sem for duplicate measurements.

25 Figures 3A-3C show that aptamer 9.3t (SEQ ID NO:70) inhibits FIXa activity in pigs.

Figure 3A is a plot showing *in vitro* anticoagulant activity of aptamer 9.3^t in porcine plasma. ■, 9.3^t APTT; □, 9.3^t PT; ●, 9.3^{tM} APTT; O, 9.3^{tM} PT. Data is presented as the mean±sem.

30 Figure 3B is a line graph showing *in vivo* anticoagulant activity of aptamer 9.3t in pigs following IV bolus injection, Activated Clotting Time (ACT) assays. ■, 1.0 mg/kg 9.3^t; □, 0.5 mg/kg 9.3^t; ●, 1.0 mg/kg 9.3^{tM}; O, Vehicle. Data is presented as the mean±sem. The ACT increase is the ratio of the

(pre-injection ACT/post injection ACT) for each time point, 1.0=no change (time 0=pre-injection).

Figure 3C is a plot showing *in vivo* anticoagulant activity of aptamer 9.3t in pigs following IV bolus injection, Prothrombin Time (PT) and activated Partial Thromboplastin Time (aPTT) assays. ■, 1.0 mg/kg 9.3^t; □, 0.5 mg/kg 9.3^t; ●, 1.0 mg/kg 9.3^{tM}; O, Vehicle. Data is presented as the mean±sem. The increase in the PT or APTT is the ratio of the (pre-injection clot time/post injection clot time) for each time point, 1.0=no change (time 0=pre-injection).

Figure 4A is a line graph showing *in vitro* inhibitory activity of cholesterol modified aptamer 9.3^t (SEQ ID NO:70 – cholesterol modified form referred to herein as 9.3^{t-C}). Cholesterol addition has modest effect on the affinity of aptamer 9.3^{t-C} for FIXa based upon a competition binding assay to measure affinity of 9.3^{t-C} for FIXa. Competitors: ■, 9.3^t; O, 9.3^{t-C}; Δ, 9.3^{tM}.

Figure 4B is a plot depicting *in vitro* anticoagulant activity of aptamer 9.3^{t-C} in human plasma. ■, 9.3^{t-C} APTT; □, 9.3^{t-C} PT; ●, 9.3^{tM-C} APTT; O, 9.3^{tM-C} PT

Figure 4C is a plot depicting *in vitro* anticoagulant activity aptamer 9.3t-C in pig plasma. ■, 9.3^{t-C} APTT; □, 9.3^{t-C} PT; ●, 9.3^{tM-C} APTT; O, 9.3^{tM-C} PT.

Figures 5A-5C depict *in vivo* anticoagulant activity of aptamer 9.3^{t-C}.

Figure 5A is a line graph showing *in vivo* anticoagulant of aptamer 9.3^{t-C} in pigs following IV bolus injection, ACT assays. ■, 0.5 mg/kg 9.3^{t-C}; □, 0.5 mg/kg 9.3^{tM-C}; dotted line is 9.3^t ACT data at 0.5 mg/ml from Figure 3B. Data is presented is the average of duplicate measurements at each time point.

Figure 5B is a plot showing *in vivo* plasma concentration of 9.3^{t-C} (solid circle) versus 9.3^t (solid square) over time following bolus IV injection. Concentrations calculated by interpolation from *in vitro* dose response curves of APTT assays for each aptamer.

Figure 5C is a plot showing *in vivo* anticoagulant of aptamer 9.3^{t-C} in pigs following IV bolus injection, APTT and PT assays. 0.5 mg/kg 9.3^{t-C}; 0.5 mg/kg 9.3^{tM-C}; * 0.5 mg/kg 9.3^t from Figure 3C; ■, 9.3^{t-C} APTT; □, 9.3^{t-C} PT; ●, 9.3^{tM-C} APTT; O, 9.3^{tM-C} PT. Data is presented is the average of duplicate measurements at each time point.

Figure 6A depicts sequences (SEQ ID NO: 23-30 and 73) of RNA aptamers that bind to and inhibit the activity of coagulation factor X and/or its

activated form factor FXa.

Figure 6B depicts sequence (SEQ ID NOS: 31-38) of RNA aptamners that bind to and inhibit the activity of coagulation factor X and/or its activated form factor FXa.

Figure 7A is a plot of data points depicting that RNA 10.14 (SEQ ID NO:73) inhibits the FXa/FVa catalyzed activation of prothrombin, thereby demonstrating that RNA 10.14 inhibits the activity of coagulation factor Xa. Factor Xa (0.5 nM) was equilibrated with no RNA (▲), 100 nM control RNA (■), or 100 nM RNA 10.14(●; SEQ ID NO:73). The prothrombin activation reaction was initiated by the addition of FVa (1 nM), PC/PS vesicles (100 µM) and prothrombin (200 nM), and the amount of thrombin formed over time at 37 C was measured.

Figure 7B is a bar graph depicting clotting time, thereby depicting that RNA 10.14 inhibits the activity of coagulation factor Xa The clotting time of normal human plasma was measured in a PT assay in the absence of RNA (striped bar), or in the presence of increasing concentrations of control RNA (solid bar) or RNA 10.14 (open bar). The clotting time is expressed as the mean ± sem for duplicate measurements.

Figure 8 is a PHOSPHORIMAGER® (Molecular Dynamics of Sunnyvale, California) scan depicting initial condition matrix to coagulation factor VIIa. Radiolabeled 2'fluoropyrimidine-modified library RNA was incubated with varying concentrations of coagulation factor VIIa in 9 different buffers, and target-bound versus free RNA was determined using the double-filter nitrocellulose filter binding assay (Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432).

Figure 9 is a PHOSPHORIMAGER® (Molecular Dynamics of Sunnyvale, California) scan of an initial condition matrix to coagulation factor IXa. Radiolabeled 2'fluoropyrimidine-modified library RNA was incubated with varying concentrations of coagulation factor IXa in 6 different buffers, and target-bound versus free RNA was determined using the double-filter nitrocellulose filter binding assay.

Figure 10 depicts sequences (SEQ ID NOS:39-47) of RNA aptamers that bind to and inhibit the activation of coagulation factor VIIa.

Figure 11 is a table depicting full-length thrombin aptamer sequences (SEQ ID NOs:50-56) produced by the toggle SELEX method of the present invention. The noted sequences are proceeded 5' by the following sequence: GGGAGAGAGGAAGAGGGAUGGG (SEQ ID NO: 48); and the noted

5   sequences are followed 3' by the following sequence: CAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC (SEQ ID NO: 49).

Figure 12 is a bar graph depicting human platelet activation by 1 nM human thrombin, in the presence of 30 nM TOG 25 RNA aptamer (SEQ ID NO: 55) or 30 nM nitrocellulose-control aptamer.

10   Figure 13 is a bar graph depicting pig platelet activation by 2 nM pig thrombin, in the presence of 25 nM TOG 25 aptamer (SEQ ID NO: 55) or 25 nM nitrocellulose binding control aptamer.

Figure 14 is a line graph depicting activated partial thromboplastin time assays that were performed on pig (solid diamonds) and human (solid

15   squares) plasma in the presence of increasing concentrations of TOG 30 aptamer (SEQ ID NO: 56). Control aptamer had no effect on APTT at these concentrations.

Figure 15 is a schematic of a proposed structure of a 25-MER truncate of TOG 25 (TOG 25 short, SEQ ID NO: 57). The "wild-type" truncate binds

20   human thrombin with a K_d of about 1 nM. The binding affinity of various mutants designed to disrupt the stem (no stem, SEQ ID NO: 58), BULGE (BULGE Us, SEQ ID NO: 59), and loop sequence (loop U1, SEQ ID NO: 60, and loop U2, SEQ ID NO: 61) are also shown.

Figure 16 is a line graph depicting activation of human platelets by 1

25   nM human thrombin in the presence of increasing concentrations of full length TOG 25 (TOGFL, SEQ ID NO:55, solid diamonds), truncated TOG 25 (TOG 25 short, SEQ ID NO: 57, solid squares), or a non-binding mutant truncate (BULGE Us, SEQ ID NO: 59, solid triangles).

Figure 17 depicts sequences (SEQ ID NOs:64-69) of RNA aptamers

30   that bind to and inhibit the activity of E2F. The aptamers were produced after 10 rounds of the SELEX method and each primer includes an oligonucleotide sequence (SEQ ID NO:62) at the 5' end and at the 3' end (SEQ ID NO:63) as noted. In Figure 17, and in other parts of the application, if a T is observed in an RNA sequence it should be construed as a U, in that the inclusion of the T

is an unintended artifact of a sequencing approach.

Figure 18 is a table depicting the alignment of a family of FIX/FIXA aptamers of the present invention and depicting a proposed secondary structure of truncated form 9.3^t (SEQ ID NO:70) of aptamer 9-3 (SEQ ID NO: 3) of Figure 1. In Figure 18, **S1** equals stem 1, **L1** equals loop 1, **S2** equals stem 2, **L2** equals loop 2, and **L3** equals loop 3.

Figure 19A is a line graph depicting that RNA 16.3 (SEQ ID NO: 41) inhibits the FVIIa/TF catalyzed activation of FX. Factors VIIa and X were equilibrated with no RNA (□), 1 µM RNA 16.3 m4 (■), or 1 µM RNA 16.3 (▲). The FX activation reaction was initiated by the addition of lipidated tissue factor, and the amount of FXa formed over time at 25°C was measured. The amount of FXa formed over time is expressed as the mean ± sem for three more experiments.

Figure 19B is a bar graph that depicts that RNA 16.3 (SEQ ID NO: 41) prolongs the tissue factor induced clotting time of human plasma. The clotting time of normal human plasma was measured in a PT assay in the absence of RNA (striped bar), wherein the presence of varying concentrations of 16.3 m4 (solid bar) or RNA 16.3 (open bar). The clotting time is expressed as the mean ± SEM for duplicate experiments.

Figure 20 depicts the secondary structure of coagulation factor IXa RNA aptamer 9.3^t (SEQ ID NO:70). The A - G substitutions that are used to create the mutant control aptamer 9.3^{tM} (K_D for factor IXa >> 5 µM) are also shown. **S1** equals stem 1, **L1** equals loop 1, **S2** equals stem 2, **L2** equals loop 2, and **L3** equals loop 3.

Figure 21 depicts the secondary structure of the minimal form of the coagulation FXa aptamer 11.F7^t (SEQ ID NO: 148) that retains full binding and inhibitory activity. Secondary structure was predicted by a combination of comparative sequence analysis and RNA folding algorithms.

Figure 22A is a histogram showing prothrombin time (PT) clotting assays in human plasma that demonstrate the anticoagulant activity of 11.7F^t (SEQ ID NO: 148). Dashed lines in histogram represents baseline clotting times in the presence of non-FXa binding control aptamers of similar length.

Figure 22B is a histogram showing activated partial thromboplastin time (APTT) clotting assays in human plasma that demonstrate the

anticoagulant activity of 11.F7^t (SEQ ID NO: 148). Dashed lines in histogram represents baseline clotting times in the presence of non-FXa binding control aptamers of similar length.

Figures 23A and 23B depict binding and inhibitory activity of FVIIa aptamers 10.15 (SEQ ID NO:75, solid squares) and 11.12 (SEQ ID NO:88, solid diamonds).

Figure 23A is a line graph showing homologous competition binding assays that demonstrate high affinity binding of both aptamers to FVIIa.

Figure 23B is a plot showing prothrombin time (PT) clotting assays in human plasma that demonstrate the anticoagulant activity of both aptamers. PT's normalized to a baseline measurements (baseline = ~12 sec.) in absence of aptamer, therefore a value of 1=no effect.

Figure 24 is a line graph wherein direct binding (corrected fraction bound (FB)) of ANG9-4 RNA aptamer (SEQ ID NO:151) is plotted as a function of protein concentration. ANG9-4 binds Ang1 (solid circles) with a K_d of ~10 nM and binds the related antagonist Ang2 with a K_d of >1 μM (>100-fold specificity)(solid triangles).

Figure 25 depicts a Western blot and table that were prepared to determine whether ANG9-4 binding inhibited Ang1 activity. 293 cells expressing human Tie2 were incubated with 13 nM Ang1* with or without a molar excess of 9-4 or control aptamer. ANG9-4 completely abrogated Tie2 autophosphorylation as detected by Western blotting with an antibody specific for phospho-Tie2 (pTie2).

Figure 26 is a histogram and table showing effect on apoptosis of Ang1 apatmers. Cultured human endothelial cells were serum-starved and treated with TNFα (50 ng/ml) for 3 hours while being incubated with 3.5 nM Ang1* and either ANG9-4 or control aptamer. Apoptosis (DNA fragmentation) was measured by Cell Death Detection ELISA kit (Roche Molecular Biochemicals). ANG9-4, but not control aptamer, increased apoptosis in a dose-dependent manner. Neither 9-4 nor control RNA increased apoptosis in un-starved, un-treated cells.

Figure 27 is a line graph wherein direct binding (corrected fraction bound (FB)) of ANG11-1 RNA is plotted as a function of protein concentration.

ANG11-1 binds Ang2 (solid triangles) with a K_d of <10 nM and binds Ang1* with a K_d of ~1 µM (>100-fold specificity)(solid circles).

Figure 28 is a histogram and table showing effect on apoptosis of Ang2 apatmers. Cultured human endothelial cells were serum-starved and treated with TNFα (50 ng/ml) for 3 hours while being incubated with 15 nM Ang2 and either ANG11-1 or control aptamer. Apoptosis (DNA fragmentation) was measured by Cell Death Detection ELISA kit (Roche Molecular Biochemicals). ANG11-1, but not control aptamer, increased apoptosis to a levels above those seen in the absence of exogenous Ang2, suggesting inhibition of both exogenous and endogenous (autocrine) Ang2, which is known to be released by endothelial cells. Neither ANG11-1 nor control RNA increased apoptosis in non-irradiated cells.

Figure 29 is a line graph wherein the ability of ANG11-1 and a 41-nucleotide truncate (ANG11-1.41) to compete for binding to ANG2 (normalized to binding in the absence of competitor) is plotted as a function of competitor concentration. ANG11-1.41 (solid squares) competes for ANG2 binding with an affinity (K_d ~ 5 nM) only slightly worse that of the full-length RNA aptamer (~ 1 nM)(solid diamonds).

Figure 30 is a secondary structure schematic of ANG11-1.41, prepared via application of sequence alignment and RNA-folding algorithms to the predominant sequence family suggests a common stem-looped structure, which incorporated the conserved sequence motif. Scrambling the 6-nucleotide consensus loop sequence (CAGCUC > ACUCCG) disrupts the ability of the truncate to bind Ang2 (K_d > 1000 nM), as does mutation of the sequence comprising the terminal stem ((K_d ~ 1000 nM).

Figure 31 is a schematic depicting the Toggle SELEX method of the present invention. Aptamers that bind both human and porcine thrombin were selected by "toggling" the protein target between human and porcine thrombin during alternating rounds of selection.

Figures 32A-32F depict RNA pool binding. The fraction of RNA bound, corrected for nonspecific binding to nitrocellulose (Corrected FB), is plotted as a function of thrombin concentration. The binding affinities of RNA pools from the toggle selection (●, circle), human thrombin selection (■, square), and

porcine thrombin selection (♦, diamond) for human thrombin protein (Figures 32A, 32C, 32E) and porcine thrombin protein (Figures 32B, 32D, 32F) were compared after round 3 (Figures 32A, 32B), round 11 (Figures 32C, 32D), and round 13 (Figures 32E, 32F).

Detailed Description of the Invention

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, biochemistry, protein chemistry, and recombinant DNA technology, which are within the skill of the art. Such techniques are explained fully in the literature. See, e.g., *Oligonucleotide Synthesis* (M. J. Gait ed. 1984); *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989); and the series *Methods in Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.).

Disclosed herein are RNA aptamer molecules that modulate, and preferably, that inhibit the activities of Factor VII, IX, X and thrombin. Also disclosed herein are E2F RNA aptamers that have been shown to bind E2F family members including E2F-3 to thereby modulate the biological activity of the E2F. Also disclosed herein are RNA aptamers that have been shown to bind Ang1 and Ang2 to thereby modulate the biological activity of Ang1 and Ang2. Optionally, the aptamers are identified through a method known in the art as Systematic Evolution of Ligands by EXponential Enrichment, SELEX; preferably, the aptamers are identified by a modified or toggle SELEX methods as disclosed herein.

The RNA aptamers of the present invention preferably comprise 2'fluoro-pyrimidines to enhance resistance to nuclease degradation. The affinities of the present inventive RNA ligands for the various factors preferably range from K_ds of about 100pM to about 10nM. In addition, these RNA ligands can act as competitive inhibitors and block factors VIIa, IXa, Xa, and thrombin activity in enzymatic assays. Moreover, these RNA ligands can act as potent anticoagulants and significantly delay the clotting time of normal human plasma or the activation of platelets in response to thrombin. The RNA aptamer ligands for E2F are useful for inhibiting cell proliferation in a

number of clinical settings including but not restricted to intimal hyperplasia following bypass graft surgery. The RNA aptamers that have been shown to bind Ang1 and Ang2 to thereby modulate the biological activity of Ang1 and Ang2 can be used in the modulation of angiogenesis.

Also disclosed herein are *in vitro* selection techniques and combinatorial chemistry methods for identifying and isolating, among other ligands, RNA aptamer molecules that bind to human coagulation factor VII, VIIa, IX, IXa, X, Xa, thrombin and activated thrombin, E2F transcription factors, and Ang1 and Ang2 with high affinity and specificity.

I.   Definitions

The following terms are believed to have well-recognized meanings in the art. However, the following definitions are set forth to facilitate explanation of the invention.

As used herein, a "target" or "target molecule" refers to a biomolecule that could be the focus of a therapeutic drug strategy or diagnostic assay, including, without limitation, proteins or portions thereof, enzymes, peptides, enzyme inhibitors, hormones, carbohydrates, glycoproteins, lipids, phospholipids, nucleic acids, and generally, any biomolecule capable of turning a biochemical pathway on or off or modulating it, or which is involved in a predictable biological response. Targets can be free in solution, like thrombin, or associated with cells or viruses, as in receptors or envelope proteins. Any ligand that is of sufficient size to be specifically recognized by an oligonucleotide sequence can be used as the target. Thus, glycoproteins, proteins, carbohydrates, membrane structures, receptors, organelles, and the like can be used as the complexation targets.

A wide variety of materials can serve as targets. These materials include intracellular, extracellular, and cell surface proteins, peptides, glycoproteins, carbohydrates, including glycosaminoglycans, lipids, including glycolipids and certain oligonucleotides.

The term "ligand" as used herein refers to a molecule or other chemical entity having a capacity for binding to a target. A ligand can comprise a peptide, an oligomer, a nucleic acid (*e.g.*, an aptamer), a small molecule (*e.g.*, a chemical compound), an antibody or fragment thereof, nucleic acid-protein

fusion, and/or any other affinity agent. Thus, a ligand can come from any source, including libraries, particularly combinatorial libraries, such as the aptamer libraries disclosed herein below, phage display libraries, or any other library as would be apparent to one of ordinary skill in the art after review of

5   the disclosure of the present invention presented herein.

The term "RNA analog" is meant to refer to a polymeric molecule, which in addition to containing ribonucleosides as its units, also contains at least one of the following: 2'-deoxy, 2'-halo (including 2'-fluoro), 2'-amino (preferably not substituted or mono- or disubstituted), 2'-mono-, di- or tri-

10   halomethyl, 2'-O-alkyl, 2'-O-halo-substituted alkyl, 2'-alkyl, azido, phosphorothioate, sulfhydryl, methylphosphonate, fluorescein, rhodamine, pyrene, biotin, xanthine, hypoxanthine, 2,6-diamino purine, 2-hydroxy-6-mercaptopurine and pyrimidine bases substituted at the 6-position with sulfur or 5 position with halo or C_{1-5} alkyl groups, abasic linkers, 3'-deoxy-adenosine

15   as well as other available "chain terminator" or "non-extendible" analogs (at the 3'-end of the RNA), or labels such as ^{32}P, ^{33}P and the like. All of the foregoing can be incorporated into an RNA using the standard synthesis techniques disclosed herein.

The terms "binding activity" and "binding affinity" are meant to refer to

20   the tendency of a ligand molecule to bind or not to bind to a target. The energetics of said interactions are significant in "binding activity" and "binding affinity" because they define the necessary concentrations of interacting partners, the rates at which these partners are capable of associating, and the relative concentrations of bound and free molecules in a solution. The

25   energetics are characterized herein through, among other ways, the determination of a dissociation constant, K_d. Preferably, the K_d is established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432. Every more preferably, an aptamer of the present invention having a preferred

30   K_d value is further evaluated in an assay for effects on the target. For example, a K_i value as described herein below can be determined for the aptamer and the target.

As used herein, "specifically binding oligonucleotides", "nucleic acid ligands" or "aptamers" refer to oligonucleotides having specific binding

regions that are capable of forming complexes with an intended target molecule in an environment herein other substances in the same environment are not complexed to the oligonucleotide. The specificity of the binding is defined in terms of the comparative dissociation constants (K_d) of the aptamer for target as compared to the dissociation constant with respect to the aptamer and other materials in the environment or unrelated molecules in general. Typically, the K_d for the aptamer with respect to the target will be 2-fold, preferably 5-fold, more preferably 10-fold less than K_d with respect to target and the unrelated material or accompanying material in the environment. Even more preferably the K_d will be 50-fold less, more preferably 100-fold less, and more preferably 200-fold less.

The binding affinity of the aptamers herein with respect to targets and other molecules is defined in terms of K_d. The value of this dissociation constant can be determined directly by well-known methods, and can be computed even for complex mixtures by methods such as those, for example, set forth in Caceci, M., et al., *Byte* (1984) 9:340-362. It has been observed, however, that for some small oligonucleotides, direct determination of K_d is difficult, and can lead to misleadingly high results. Under these circumstances, a competitive binding assay for the target molecule or other candidate substance can be conducted with respect to substances known to bind the target or candidate. The value of the concentration at which 50% inhibition occurs (K_i) is, under ideal conditions, equivalent to K_d. However, in no event will a K_i be less than K_d. Thus, determination of K_i, in the alternative, sets a maximal value for the value of K_d. Under those circumstances where technical difficulties preclude accurate measurement of K_d, measurement of K_i can conveniently be substituted to provide an upper limit for K_d. A K_i value can also be used to confirm that an aptamer of the present binds a target.

As specificity is defined in terms of K_d as set forth above, in certain embodiments of the present invention it is preferred that excluded from the categories of unrelated materials and materials accompanying the target in the target's environment are those materials which are sufficiently related to the target to be immunologically crossreactive therewith. By "immunologically crossreactive" is meant that antibodies raised with respect to the target crossreact under standard assay conditions with the candidate material.

Generally, for antibodies to crossreact in standard assays, the binding affinities of the antibodies for crossreactive materials as compared to targets should be in the range of 5-fold to 100-fold, generally about 10-fold.

In general, aptamers preferably comprise about 10 to about 100 nucleotides, preferably about 15 to about 40 nucleotides, more preferably about 20 to about 40 nucleotides, in that oligonucleotides of a length that falls within these ranges are readily prepared by conventional techniques. Optionally, aptamers can further comprise a minimum of approximately 6 nucleotides, preferably 10, and more preferably 14 or 15 nucleotides, that are necessary to effect specific binding. The only apparent limitations on the binding specificity of the target/oligonucleotide couples of the invention concern sufficient sequence to be distinctive in the binding oligonucleotide and sufficient binding capacity of the target substance to obtain the necessary interaction. Aptamers of binding regions containing sequences shorter than 10, e.g., 6-mers, are feasible if the appropriate interaction can be obtained in the context of the environment in which the target is placed. Thus, if there is little interference by other materials, less specificity and less strength of binding can be required.

As used herein, "aptamer" refers in general to either an oligonucleotide of a single defined sequence or a mixture of said oligonucleotides, wherein the mixture retains the properties of binding specifically to the target molecule. Thus, as used herein "aptamer" denotes both singular and plural sequences of oligonucleotides, as defined hereinabove. The term "aptamer" is meant to refer to a single- or double- stranded nucleic acid which is capable of binding to a protein or other molecule, and thereby disturbing the protein's or other molecule's function.

Structurally, the aptamers of the invention are specifically binding oligonucleotides, wherein "oligonucleotide" is as defined herein. As set forth herein, oligonucleotides include not only those with conventional bases, sugar residues and internucleotide linkages, but also those that contain modifications of any or all of these three moieties.

"Single-stranded" oligonucleotides, as the term is used herein, refers to those oligonucleotides that contain a single covalently linked series of nucleotide residues.

"Oligomers" or "oligonucleotides" include RNA or DNA sequences of more than one nucleotide in either single chain or duplex form and specifically includes short sequences such as dimers and trimers, in either single chain or duplex form, which can be intermediates in the production of the specifically binding oligonucleotides. "Modified" forms used in candidate pools contain at least one non-native residue.

"Oligonucleotide" or "oligomer" is generic to polydeoxyribonucleotides (containing 2'-deoxy-D-ribose or modified forms thereof), i.e., DNA, to polyribonucleotides (containing D-ribose or modified forms thereof), i.e., RNA, and to any other type of polynucleotide which is an N-glycoside or C-glycoside of a purine or pyrimidine base, or modified purine or pyrimidine base or abasic nucleotides.

An "RNA aptamer" is an aptamer comprising ribonucleoside units. "RNA aptamer" is also meant to encompass RNA analogs as defined herein above.

The term "coagulation factor aptamer" is meant to refer to a single- or double-stranded nucleic acid that binds a coagulation factor and modulates its function. The term "coagulation factor" is meant to refer to a factor that acts in either or both of the intrinsic and the extrinsic coagulation cascade.

When a number of individual, distinct aptamer sequences for a single target molecule have been obtained and sequenced as described above, the sequences can be examined for "consensus sequences". As used herein, "consensus sequence" refers to a nucleotide sequence or region (which might or might not be made up of contiguous nucleotides) that is found in one or more regions of at least two aptamers, the presence of which can be correlated with aptamer-to-target-binding or with aptamer structure.

A consensus sequence can be as short as three nucleotides long. It also can be made up of one or more noncontiguous sequences with nucleotide sequences or polymers of hundreds of bases long interspersed between the consensus sequences. Consensus sequences can be identified by sequence comparisons between individual aptamer species, which comparisons can be aided by computer programs and other tools for modeling secondary and tertiary structure from sequence information.

Generally, the consensus sequence will contain at least about 3 to 20 nucleotides, more commonly from 6 to 10 nucleotides.

As used herein "consensus sequence" means that certain positions, not necessarily contiguous, of an oligonucleotide are specified. By specified it is meant that the composition of the position is other than completely random. Not all oligonucleotides in a mixture can have the same nucleotide at such position; for example, the consensus sequence can contain a known ratio of particular nucleotides. For example, a consensus sequence might consist of a series of four positions wherein the first position in all members of the mixture is A, the second position is 25% A, 35% T and 40% C, the third position is T in all oligonucleotides, and the fourth position is G in 50% of the oligonucleotides and C in 50% of the oligonucleotides.

The terms "cardiovascular disease" and "cardiovascular diseases" are meant to refer to any cardiovascular disease as would be understood by one of ordinary skill in the art. Examples of particularly contemplated cardiovascular diseases include, but are not limited to, atherosclerosis, thrombophilia, embolisms, cardiac infarction (e.g., myocardial infarction), thromboses, angina, stroke, septic shock, hypertension, hyper-cholesterolemia, restenosis and diabetes. More particularly, the terms "cardiovascular disease" and "cardiovascular diseases" are meant to refer to cardiovascular diseases in which thrombosis plays a causative, aggravating and/or indicating role.

The phrase "treating cardiovascular disease" is meant to refer to the treatment of cardiovascular disease at any stage of progression. Thus, treatment of early onset cardiovascular disease as well as treatment of advanced cardiovascular disease falls within the scope of the phrase "treating cardiovascular disease". The phrase "treating cardiovascular disease" is also meant to refer to a therapeutic method directed toward inhibiting the aggravation of cardiovascular disease by modulating coagulation.

The term "truncate" refers to an aptamer that has been truncated by deletion of nucleotides but still possesses a desired or even improved binding characteristic. Truncates can vary in length in accordance with the length of the starting aptamer and as defined above for the term "aptamer".

Truncations in the truncate can occur in fixed or variable regions, or both fixed and variable regions, of the starting aptamer.

The term "about", as used herein when referring to a measurable value such as an amount of weight, time, dose, etc. is meant to encompass variations of ±20% or ±10%, more preferably ±5%, even more preferably ±1%, and still more preferably ±0.1% from the specified amount, as such variations are appropriate to perform the disclosed method.

Following long-standing patent law convention, the terms "a" and "an" mean "one or more" when used in this application, including the claims.

II. RNA Aptamers

An RNA aptamer that selectively binds a coagulation pathway factor, that selectively binds an E2F family member, or that that selectively binds Ang1 or Ang2 is provided in accordance with the present invention. Preferably, the binding affinity for the RNA aptamer for the coagulation pathway factor is represented by dissociation constant of about 20 nanomolar (nM) or less, more preferably about 10 nanomolar (nM) or less. Optionally, the coagulation pathway factor is selected from the group including but not limited to prothrombin, thrombin, IX, IXa, X, Xa, VII, VIIa, V, Va, VIII, VIIIa, tissue factor, XI, XIa and combinations thereof. Most preferably, the RNA aptamers bind activated coagulation factors.

Thus, improved nucleic acid ligands to coagulation factors, to E2F family members, and to Ang1 or Ang2 are disclosed and claimed herein. This invention includes the specific nucleic acid ligands identified herein. The scope of the ligands covered by the invention extends to all ligands of a coagulation factor, to E2F family members, and to Ang1 or Ang2 identified according to the procedures described herein. More specifically, this invention includes nucleic acid sequences that are substantially homologous to and that have substantially the same ability to bind coagulation factors, E2F family members, or Ang1 or Ang2, under physiological conditions, as the nucleic acid ligands identified herein. By substantially homologous, it is meant, a degree of homology in excess of 70%, most preferably in excess of 80%. Alignment techniques are disclosed herein below. Substantially homologous also includes base pair flips in those areas of the nucleic acid ligands that

include base pairing regions. Substantially the same ability to bind a coagulation factor, an E2F family member, or Ang1 or Ang2 means that the affinity is within two orders of magnitude of the affinity of the nucleic acid ligands described herein. It is well within the skill of those of ordinary skill in the art to determine whether a given sequence is substantially homologous to and has substantially the same ability to bind a coagulation factor, an E2F family member, or Ang1 or Ang2 as the sequences identified herein.

II.A.   Coagulation Factor IX Aptamers

In one embodiment, an RNA aptamer of the present invention selectively binds an activated coagulation factor IXa (FIXa) or inactive form thereof, i.e. (Factor IX).   Preferably, the dissociation constant ranges from about 100 pM to about 10 nM.   More preferably, the dissociation constant ranges from about 400 pM to about 10nM, and can optionally comprise any value within the range, e.g. about 500 pM, about 600 pM, about 700 pM, about 800 pM, about 900 pM, about 1 nM, about 2.5 nM, or about 5 nM.   Even more preferably, the K_d is established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432.

Referring now to Figs. 1A-1B, representative sequences of RNA aptamers of the present invention that bind to and inhibit the activity of FIXa are disclosed. In a preferred embodiment of each of the sequences of Figs. 1A-1B, all cytidines are 2'-deoxy-2' fluoro cytidine and all uridines are 2'-deoxy-2'-fluorouridine. Binding data for the aptamers of Figs. 1A and 1B are presented in Tables 1 and 2.

TABLE 1

Affinities (expressed as apparent dissociation constants) of FIX/FIXa
Aptamers for FIXa as determined by
Double-Filter Nitrocellulose Filter Binding Assays

Sequence	K_d (pM)	SEQ ID NO:
9.3	500-700	3
9.19	500-1000	16
9.20	400-600	17

9.25	400-600	19
9.26	400-600	20
9.27	1500-1800	21
9.28	500-700	22

TABLE 2

Primary sequence of the minimal or truncated FIXa aptamers 9.3^t and 9.20^{t*}

9.3^t: 5' AUG GGG ACU AUA CCG CGU AAU GCU GCC UCC CCA U 3'

(SEQ ID NO: 70)

9.20^t: 5' GGG GAC UAU ACC GGC AAU CGU GCA UCC CC 3'

(SEQ ID NO: 71)

The apparent K_d of the 9.20 truncate for FIXa is ~100-200 nM. The apparent K_d for binding of the 9.3 truncate to FIXa and to FIX is described in Table 3 immediately below.

TABLE 3 - Aptamers to Coagulation Factor IXa

Aptamer

Protein	9.3	9.3^t	9.3^{tM}
Factor IXa	0.65±0.2 nM	0.58±0.05 nM	>10 μM
Factor IX	3.96±0.7 nM	4.7±0.8 nM	n.d.
Factor VIIa	n.d.	> 5 μM	n.d.
Factor Xa	n.d.	>5 μM	n.d.
Factor XIa	n.d.	>5 μM	n.d.
APC	n.d.	>5 μM	n.d.

Table 3 shows affinity of 9.3 and related aptamers to FIXa and other coagulation factors; 9.3 is a full-length aptamer, while 9.3t is a 35 nucleotide truncated version of 9.3.

Referring now to Figures 18 and 20, an alignment of FIX/FIXA aptamers of the present invention is presented, along with a proposed

secondary structure of truncated aptamer 9-3^t (SEQ ID NO: 70). As shown in Figures 18 and 20, the alignment of the FIX/FIXA aptamers suggest a first stem region **S1** followed by a first loop region **L1**, and then a second stem region **S2** and a second loop region **L2**. A third loop region **L3** is also suggested. The motif AUA is common in the **L1** region and thus, preferably, a FIX/FIXA aptamer of the present invention comprises the AUA motif. Thus AUA motif thus comprises a consensus sequence for this family of aptamers. Additionally, in the 5' direction, it is preferred that 2 additional nucleotides are present, and the nucleotides N in the 5' direction can be selected from the group including but not limited to C, U, G, A and identical combinations thereof. Thus, the sequence NNAUA is also a consensus sequence for this family of aptamers.

Continuing with Figs. 18 and 20, it is also preferred that the **S1** region preferably comprises about 5 nucleotides at the 5' end that form base pairs with about 5 base pairs at the 3' end to maintain the stem structure. By "pair forming" it is simply meant the ordinary complimentary base pair formation found in RNA molecules. To elaborate, the secondary structure of an RNA motif can be represented by contact in two dimensions between specific nucleotides. The most easily recognized secondary structure motifs are comprised of the Watson/Crick base pairs A:U and C:G. Non-Watson/Crick base pairs, often of lower stability, have been recognized, and include the pairs G:U, A:C, G:A, and U:U. (Base pairs are shown once; in RNA molecules the base pair X:Y by convention represents a sequence in which X is 5' to Y, whereas the base pair Y:X is also allowed.) A conventional nomenclature for the secondary structures thus includes stems, loops, hairpin loops, asymmetric bulged hairpin loops, symmetric hairpin loops, and pseudoknots.

II.B.   Coagulation Factor VII Aptamers

In another embodiment, an RNA aptamer of the present invention selectively binds activated coagulation factor VII (FVIIa) or an inactive form thereof, i.e. (Factor VII). Preferably, the dissociation constant ranges from about 100 pM to about 10 nM. More preferably, the dissociation constant ranges from about 400 pM to about 10nM, and can optionally comprise any value within the range, e.g. about 500 pM, about 600 pM, about 700 pM,

about 800 pM, about 900 pM, about 1 nM, about 2.5 nM, or about 5 nM. Even more preferably, the K_d is established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432.

5   Referring now to Fig. 10, representative sequences of RNA aptamers of the present invention that bind to and inhibit the activity of coagulation factor FVIIa are disclosed. In a preferred embodiment of each of the sequences of Figure 10, all cytidines are 2'-deoxy-2' aminocytidine and all uridines are 2'-deoxy-2'-aminouridine. Binding data for the aptamers of Fig.

10   10 are presented in the Laboratory Examples.

Table 4 shows additional sequences of RNA aptamers isolated to coagulation factor VIIa. Shown are the random-region derived sequences (5' to 3') of aptamers resulting from the selection against FVIIa. In a preferred embodiment, all pyrimidines are 2'fluoro-modified. The random region

15   derived sequences are flanked by fixed sequences from the library as shown: 5' gggagagaggaagagggauggg (SEQ ID NO:102) -random region- cauaacccagaggucgau 3' (SEQ ID NO:103). Binding data for the aptamers of Table 4 are presented in the Laboratory Examples. In Table 4, the numerals "10" and "11" refer to the fact the aptamer was isolated after ten (10) rounds

20   or eleven (11) rounds of SELEX, respectively.

Table 4
FVII/FVIIa Aptamers

SEQ ID NO:	SELEX ROUND AND SPECIE	Random Region of Aptamer Sequence
74	11-15	AAAGUACCGACUAGGUCCCACUGUUUAAGCAUCCCCGAAC
75	10-15	AAGCUCCAUCCAAGCGACGACACGCUCGUCCCGAAAAGAAU
76	10-1,	
	10-5,	
	11-19	AAGCUCCGUCCAAGCGACGACACGUUCGUCCCGAAAAGAAU
77	11-6,	
	11-27	ACAACGCCACCUUCCGCGCGACGCCGCGCCGACGAUAACU
78	10-7	ACAACGCCACCUUCCGCGCGACGCCGCGCCGACGUAUAACU
79	11-1	ACGAAAAUAUCUCCGUCAAGGACCUCCUGCCCCAAACACU
80	11-17	AGACGACACAUCCAAGCGUGAGAGAUCACCCGACAAGAAU

81 11-20AUUUUUUCACACAUUCUUAAUUUUCACUUACCCGUCCCGAUC

82 10-9 CAAAGCACCCGUCCAAGCGACAGACAUGUCCCGCAGCCCU

83 10-13 CACCAUUUAUUCUUCAUUUUUCUUCGCCCAGUUCCUCCAA

84 10-14 CAUAAGCCGCCUCAGCUGACAAAGCCCUCCGCUUAGGCC

85 11-23 CCAAAGUGCUUCCGCGAAGUUCGACCAUUCGCCGCCUGCA

86 10-11 CCCCUCCGCCAACUUGGCCGCCUCAGGCACCAUCACCAAC

87 10-2 CCCGAUCUCCCCGAGGACCUCCACGGCCCGUCCGCCAGUUU

88 11-3 CCGCCUCAGCAAUCUAGCCCUCCGCCCGACCCUUCCGCUG

89 11-12,

11-13 CCGCCUCAGCGAGAUCUUCGCCCUCCGCCCAAGCCUCAAC

90 11-25 CCGCCUCAGGACGACACCGGUCCCCUCCGCCCGUCCGCGC

91 10-3 CCGCCUCAGGCAUCAGCCCCUCCGCCCGCCCACUUCAUCA

92 10-12 CCGCCUCAGUUACUUGAUAACCCUCCGCCCGCCCGCAGCU

93 11-18 CUUUACAUAUUACUUACUACAUUUUCAUAACACCACACGC

94 11-7 GACACCAUCCAAGCGACCAACCAAGGUCCCGCACAUAACU

95 10-10 GAUGCAACUCGAAAUGGCCGCCUCGCGUCAGCGUUCCGC

96 10-4 GCUUAUCUUAUAUCACUUUUUCUUCCCAAUCCUUCAAGU

97 10-6,

98 11-5 UAACCAACCAAGCGUCCAAAAACCUGGACCCGCCAAGAAU

99 11-14 UAACCAACCAAGCGUCCAAAAAUCUGGACCCGCCAAGAAU

100 11-10 UCUGACGUUCCACCGUCCUCGAAGGCGACCAGAGCGUUAC

101 11-8,

11-16 UGCCGCCUCAGCCACACGGCCCUCCGCGCCCGCCACAAGC

II.C. Coagulation Factor X Aptamers

In another embodiment, an RNA aptamer of the present invention selectively binds activated coagulation factor Xa (FXa) or an inactive form thereof, i.e. (Factor X). Preferably, the dissociation constant ranges from about 100 pM to about 10 nM. More preferably, the dissociation constant ranges from about 400 pM to about 10nM, and can optionally comprise any value within the range, e.g. about 500 pM, about 600 pM, about 700 pM, about 800 pM, about 900 pM, about 1 nM, about 2.5 nM, or about 5 nM. Even more preferably, the K_d is established using a double-filter nitrocellulose filter binding assay such as that disclosed by Wong and Lohman, 1993, *Proc. Natl.*

Acad. Sci. USA 90, 5428-5432.

Referring now to Figs. 6A-6B, representative sequences of RNA aptamers of the present invention that bind to and inhibit the activity of FXa are disclosed. In a preferred embodiment of each of the sequences of Figs. 6A-6B, all cytidines are 2'-deoxy-2' fluorocytidine and all uridines are 2'-deoxy-2'-fluorouridine. Binding data for the aptamers of Figs. 6A and 6B are presented in the Laboratory Examples.

Table 5 shows additional sequences of RNA aptamers isolated to coagulation factor X/Xa. Binding data for the aptamers of Table 5 are presented in the Laboratory Examples, including Example 12. In Table 5, the numerals "10" and "11" refer to the fact the aptamer was isolated after ten (10) rounds or eleven (11) rounds of SELEX, respectively. The FXa sequences listed in table 5 are flanked by fixed sequences that are the same as the fixed sequences described in the preceding section on aptamers to factor VIIa. That is, the 5' and 3' flanking sequences are, respectively, SEQ ID NOs:102 and 103.

TABLE 5

SEQ ID SELEX Round and Specie No.			
NO:	Clone	Sequence	Kd (nM)
104	F11-8	AgAuuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuACuAC	2.2
105	D7-9	uAAAuAGCCCCAGCGAGAuucuACuuGGCCCCGCuACuAC	2.633
106	D6-6	AAAAuAcgCCannCGAGAuuAuACuuGGCCCCGCuAauAC	3.1
107	F11-7	AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuAuuAC	3.6
108	D7-6	AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuAgcAC	3.8
109	D6-2	AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuACaAC	4.6
110	D7-1	AgAAugGCCCCAGCGAGAuuAuACuuGGCCCCGCcAauAC	4.7
111	D6-1	AAAAuAGCCCCAGCGAGAugAuACuuGGCCCCGCuAauAC	4.8
112	D7-7	AgAAuAcgCCuAGCGAGAagAuACuuGGCCCCCGugCaAC	5.8
113	D6-3	AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuguuAC	5.9
114	D6-9	AAAuuuGCCCCAGCGAGAuAAuACuuGGCCCCGCaACuAC	6.5

			similar to 10-14
115	D4-7	AuAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuACuAa	
116	D7-2	AgAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuAauAC	8.1
117	D6-4	AAAuuuGCCCuAGCGAGAuuAuACuuGGCCCCGCgAaaaAC	8.5
118	E10-12	AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCgAacAC	11.7
119	D6-7	ugcAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuACaAC	13.2
120	D7-8	ngAuuAGCCCnAGCGAGAuAnuACuuGGCCCCGCuACnuC	14.49
121	D4-8	AAAAuAaCCaCAGCGAGAucAuACuuGGCCCCGuuACuAC	2 fold higher
122	D4-10	AAAAuAGCCCuAGCGAGAuAAuACuuGGCCCCGCcACaua	2 fold higher
123	D6-10	cAgAuAGCCaCAGCGAGAucAuACuuGGCCCCGCuACuAC	18.7
124	D4-5	AgAAuAGCCCCAGCGAGAuAAucCuuGGCCCCGCuACugC	21.66
125	D4-6	AAncuAGCCCnAGCGAGAuAuuACuuGGCCCCGCnACuAC	3 fold higher
126	D7-5	AAAcuAGCCuCAGCGAGAuAAuACuuGGCCCCGCuACuAC	26.1
127	E10-11	CCAGAAGCGCuCACuACAACGuuGAACCCCCCGuCCACAC	27.11
128	E10-8	CCAAAAGCGGACuGAAGACGuGuuuCCCCCAuCuCCGuGA	28.38
129	E9-8	CCAGAAGGAACuAAACACCuGAACCCCCCAuCGCGAGAGA	29.81
130	F11-6	CCAGCAACGuCACACGAACGGAAuACCCCCCAuuGAAAAC	33.6
131	E10-4	uCuuAGAuAuAGAACuCCGAGAGGACuGACCGuACAGAAC	37.44
132	D7-4	AgAAuAGCCCCAGCGAGAucguACuuGGCCCCGCuAguAC	39.3
133	E9-3	CCAAAAGCGCAuACACCuGCGuGuuuCCCCCGCCAACAGu	46.55
134	E10-1	CCAuuGCuNCCCuGAACANGGGCNCCACNCCGCCuNCACAGu	51.7
135	E9-9	CCAGAACACCAGuGAACCCCCCAGCCCCuuCuCACCAGAu	52.81
136	E9-5	CCAGAAGCGACACuAACGCuGAACCCCCCAGuCCCuuCACGuG	53.5
137	E9-2	AuACCGAGCACGCAAAACACACAAuGCCCAAGCAGGACu	58.6
138	E9-4	AGCCCGAGAAAuAACGCGuuCCACCAuACuACuAAGC	65
139	D4-3	uAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCaACuAC	65.5
140	E10-7	AGuCCGACuGGAGAACANGuACuCuAuAAGCACuuNCAuNCAN	69.45
141	F11-10	CuCGGCAGAAGACACGCAuuCACCuGGuGCCACCuCGuAA	84.43
142	E10-6	GCCGuCGCCAGGAAuCAAACuGCuACuCCAuCCCGGGCA	85.7
143	E9-6	CCAGAAGCuAAACACuCAuAACCACGCuGAACCCCCCAAC	95.1
144	E9-10	CCAGAACCAACuGCGGuGAACCCCCCAuACCGCGACACAu	130.4
145	D4-2	AAcuuAGCCuCAGCGAGAuAAcgCuuGGCCCCGCuAagAC	540

| 146 | D4-9 | uAAguuGCCCCAGCGAGAuAguACuuGGCCCCGCuACuAa | >240 |
| 147 | E9-1 | AAAAuAGCCCCAGCGAGAuAAuACuuGGCCCCGCuACuAA | |

II.D. Thrombin Aptamers

In another embodiment, an RNA aptamer of the present invention
selectively binds coagulation factor thrombin (activated) (Factor IIa (FIIa)), or
an inactive form thereof (i.e. prothrombin, factor VII). Preferably, the
dissociation constant ranges from about 100 pM to about 10 nM. More
preferably, the dissociation constant ranges from about 400 pM to about
10nM, and can optionally comprise any value within the range, e.g. about 500
pM, about 600 pM, about 700 pM, about 800 pM, about 900 pM, about 1 nM,
about 2.5 nM, or about 5 nM. Even more preferably, the K_d is established
using a double-filter nitrocellulose filter binding assay such as that disclosed
by Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432.

Referring now to Figure 11, representative full-length thrombin aptamer
sequences are disclosed, along with dissociation constants (K_d) for human
and porcine thrombin. Significantly, 13 rounds of the toggle SELEX method
disclosed herein in accordance with the present invention produced these
aptamers. A preferred consensus sequence of these aptamers comprises
AACAA. A preferred embodiment of a thrombin aptamer sequences
comprises the sequence referred to as toggle 25 (TOG25; SEQ ID NO: 55). A
truncated form of this aptamer was also prepared, and the truncate is referred
to herein as TOG 25 short (SEQ ID NO: 57).

As shown in Figure 15, a thrombin RNA aptamer of the present
invention preferably comprises about 3 pair forming nucleotides followed by
the AACAA consensus sequence and two additional pair forming nucleotides.
As shown in Fig. 15, the pair forming nucleotides form pairs with
complementary nucleotides proximate to the 3' end of the TOG 25 short
aptamer.

II.E. E2F Aptamers

In another embodiment, an RNA aptamer of the present invention
selectively binds E2-F, also referred to as "an E2F family member". Thus, the

terms "E2-F" and "E2-F family member" encompass any E2F family member, whether now known or hereafter identified. Representative E2F family members include but are not limited to E2F-1, E2F-2, E2F-3, E2F-4, E2F-5 and E2F-6. Preferably, the dissociation constant ranges from about 100 pM

5   to about 50 nM. More preferably, the dissociation constant ranges from about 400 pM to about 10nM, and can optionally comprise any value within the range, e.g. about 500 pM, about 600 pM, about 700 pM, about 800 pM, about 900 pM, about 1 nM, about 2.5 nM, about 5 nM, or about 10 nM. Even more preferably, the K_d is established using a double-filter nitrocellulose filter

10   binding assay such as that disclosed by Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432.

Referring now to Fig. 17, representative sequences of RNA aptamers (SEQ ID NO: 62-69) that bind to and inhibit the activity of E2F family members including E2F-3 are disclosed. Each of the aptamers (SEQ ID NO: 64-69) are

15   preferably bounded at their 5' end by the 5 primer sequence **5'P** of SEQ ID NO: 62 and are preferably bounded at their 3' end by the 3 primer sequence **3'P** of (SEQ ID NO: 63). These primers were identified after 10 rounds of SELEX wherein the SELEX method was modified in accordance with the matrix conditions described in Examples 1 and 2. The approximate K_d's for

20   these aptamers are set forth in Table 6.

Table 6A

Approximate K_d's for E2F Aptamers

Aptamer No.	SEQ ID NO.	K_d
10-1 and 10-8	64	1.5 nM
10-2	65	3 nM
10-3, 10-7, 10-11 and 10-12	66	1 nM
10-4	67	5 nM
10-5	68	2.5 nM
10-6	69	2 nM

25   Thus, RNA aptamer ligands that selectively bind to an E2F family member, e.g. E2F-3, are disclosed herein. Among other utilities as disclosed

herein, these aptamers have utility in the control of cell proliferation, which is of central importance to the proper development of a multi-cellular organism, the homeostatic maintenance of tissues, and the ability of certain cell types to respond appropriately to environmental cues. E2F is a family of transcription factors and modulation of E2F activity is envisioned to be particularly effective in repeating a wide variety of proliferative events in view of the control of E2F activity occurring as the end result of G_1 cyclin dependent kinase regulatory cascades that involve the Rb family of proteins. See, e.g., Sherr, C.J., *Cell*, 73:1059-1065 (1993); Hunter, T., *Cell* 75:839-841 (1993); Nevins J.R., *Science*, 258:424-429 (1992); Helin, K. and Harlow, E., *Trends Cell Biol.* 3:43-46 (1993); La Thangue, N.B., *Trends Biochem. Sci.* 19:180-114 (1994); Sherr, C.J. and Roberts, J.M., *Genes Dev.* 9:1149-1143 (1995); Weinberg, R.A. *Cell* 81:323-330 (1995) Harbour, J.W. and Dean, D.C., *Genes and Development* 14:2393-2409 (2000); and Black, A.R. and Azizkhan-Clifford, J., *Gene* 237:281-302 (1999).

Table 6B shows additional sequences of RNA aptamers isolated to an E2F family member. Shown are the random-region derived sequences (5' to 3') of aptamers resulting from the selection against E2F. In a preferred embodiment, all pyrimidines are 2'fluoro-modified. The random region derived sequences are flanked by fixed sequences from the library as shown: 5' GGG GGA AUU CUA AUA CGA CUC ACU AUA GGG AGA GAG GAA GAG GGA UGG G (SEQ ID NO:188) -random region- C AUA ACC CAG AGG UCG AUA GUA CUG GAU CCC CCC 3' (SEQ ID NO:63). Binding data in the form of K_d values are also shown.

<div align="center">

Table 6B

E2F Aptamers

</div>

SEQ ID NO:	Random Region of Aptamer Sequence	K_d
189	GCUGCCGCGCCUGGACCCCACCCACAUAUGGGCCACACAC	1.5 nM
190	AAUGACAAUUGACUCGGAAACCCUCAUGUUCCAACACCGG	
191	CCUACUCUCCACACCUGGUUUUAUGCUCUACACACCUCAC	
192	CUGCCCCGACCACAAAGGACGGAACCCUACCCACAGUGGG	
193	CAUAAAAGCAAUUUGCCACCGGCGUACGGCACCCCAAUAU	
194	CACCUAUGCCAUCAGGCCUCAAUCUCCGGCAGCGACUCUA	
195	AUCAACCACAGGAAGAGUGCAGCCAUAGCACACAGACCA	

196	GCGACAUACCCCACCCACACUGGCACAACGCGCAAUGCCG	
197	CUUCAAAGGUCCUGUAUCCAGCCACCCACUGACAGGA	
198	CUACCCAGCAAGGUCAACCCUACCCACACUGG	1.75 nM
199	AUCUUAAAGAUCACCGGCGUUCGGCAACACCCGACCCAAA	
200	GCACUAAACUUCGAUUACCCCCCACCCACACUGGCUGCAC	4 nM
201	CAGAUUACCCUACCCACACUGCGUGCGGACAACCAUUGGC	0.4 nM
202	GCACAAAUGAGAACACGAGUUCACCCCGCCCACACUGGA	
203	GCGCAGAUCAACCCUACCCAUACUGGGCUCCUUGUGAAGG	
204	CAAGCGCUGAAACCAAUGCACCCCACCCCACACUGGUGUAC	1.25 nM
205	AUGUGAAACACAGAAGCCCUGUACAGACCGCCGACUGUCA	*
206	CAAACUCACAGACACCAACUGCAGGAGCACCCACCACGAC	
207	CGAACGAACUGUGGACCCUACCCACACUGGGCCAAGCGAU	0.4 nM
208	CGCCCUGGAACGAGAUUCCUGUAAACCCCCAUCUAGUAGA	
209	CAAGGUGACCGCGAACCCUACCCGCCGCACGGUAACAGCG	
210	CAUCCAGACUACUGGCCCAACCCGCCGCUCCAACCCCGUG	
211	CUCUCUCCGUAACCAACAAGUCCCAAUGAACAACCACCAU	
212	CACUGAACGAAUGGCAACCGCCAAACCCUACCCACACUGG	*	0.2 nM
213	CAAGCGUAUACCCUACCCACACUGAGCUACAUUGCGCUGA	8 nM
214	GCCGAGAGUGAGUGACCACAACCCCGCCCACACUGGAAUA	1.5 nM
215	UUUCCUAUGGCGAUAACUUCAGCCACGCCGGCGCCCCGUG	30 nM
216	CGUCACUCCGUCCCAGCCGACGAAGUCCGUAAUUCCUCCA	45 nM
217	CCACCCGAAGCAAAUCAAGCCCGACGGCGCUCGGACCAAC	15 nM
218	CGAACUGAAGCUAGCGUAACCCUACCCACACUGCACGUG	0.5-4 nM
219	ACCUCGACCCUUCACCUGACUCUCCCAGAAGUUCUGUUUC	2 nM
220	CAAUCCAUACGCACCCGGUCCACACUGGGUUGG AGCNNN	1-40 nM
221	AAUGGAAUCACUGAAGGCCCUCCGUAGCACCUAACACAGU	*	1.5 nM
222	GCAUCCUGCCAGCGGCGACGGACCUUCGCCCACAGGCCUC	2 nM
223	UUAUAUAGCACACUGAAGCCCUCAGCAAAACCUCCACAGG	*	1.5 nM
224	UAUGAAAUCACAGAAGCCCGCGUUCGACACCUCCACUGUU	*	3 nM
225	CAAACUCACAGACUCCAACUGCAGGAGCACCCACCCACACUGGGACAG		0.25-2.5 nM
226	AUCCCCGCCGUAAGCCGUCCUGAUGGACACCACACGCCGC	*	2 nM

II.F. Angiopoietin-1 (Ang1) and Angiopoietin-2 (Ang2) Aptamers

Tie2 is an endothelial receptor tyrosine kinase (RTK) that is required for both embryonic vascular development and pathological angiogenesis. Tie2 is unique among RTKs in that it has two ligands with apparently opposing actions. Angiopoietin-1 (Ang1) is an activating ligand while Angiopoietin-2 (Ang2) is thought to be a naturally occurring antagonist for Tie2. Mice lacking Tie2 or Ang1 die midway through gestation due to

abnormalities of vascular morphogenesis characterized by deficient recruitment of supporting smooth muscle cells and pericytes. Moreover, Ang1 promotes endothelial cell survival and blocks the increases in vascular permeability induced by vascular endothelial growth factor (VEGF), supporting a role for Ang1 in the stabilization and maintenance of the adult vasculature. In contrast, Ang2 is required for VEGF-mediated angiogenesis, and in the absence of endothelial mitogens Ang2 may induce vascular regression.

The exact mechanism of action of the Angiopoietins remains to be elucidated. For example, high-dose Ang2 can induce downstream activation of Akt and endothelial cell survival, suggesting that it does not simply exert a dominant negative effect on Tie2. The need for improved understanding of these ligands' function is particularly important in the study of tumor angiogenesis, as several studies have now shown that inhibition of Tie2 with a soluble receptor blocks tumor growth, angiogenesis, and metastasis. However, it is unclear whether these effects are due to inhibition of the effects of Ang1 or Ang2, since a soluble receptor would bind both ligands. Specific inhibitors of these ligands have the potential to more precisely modulate Tie2 signaling and serve as valuable therapeutic agents. The present invention provides RNA aptamer ligands for Ang1 and Ang2.

A random library of 2'-fluoro modified RNA was created with the following sequence:

GGGAGAGAGGAAGAGGGAUGGG (SEQ ID NO:149) -N_{40}-

CAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC (SEQ ID NO:150), where N_{40} is a random region.

In vitro selection was performed using recombinant human angiopoietin-1* (ANG1*; Regeneron Pharmaceuticals, Tarrytown, New York). After 9 rounds of SELEX, the pool was cloned and sequenced, and a single random region sequence (ANG9-4-SEQ ID NO:151) was identified:

ACUCGAACAUUUCCACUAACCAACCAUACUAAAGCACCGC.

In Figure 24, direct binding (corrected fraction bound) of ANG9-4 RNA is plotted as a function of protein concentration. ANG9-4 binds Ang1 with a K_d of ~10 nM and binds the related antagonist Ang2 with a K_d of >1 µM (>100-fold specificity). Additional data pertaining to Ang1 aptamers is presented in the Laboratory Examples.

Table 7 sets forth additional representative Ang1 aptamers. Analysis of earlier SELEX rounds revealed several unique clones with random region sequences bearing similarities to ANG9-4. Aptamer sequences are as follows: GGGAGAGAGGAAGAGGGAUGGG (SEQ ID NO:149) -N_{40}-

5   CAUAACCCAGAGGUCGAUAGUACUGGAUCCCCC (SEQ ID NO:150).

Table 7

Ang1 Aptamers

SEQ ID NO:	Clone –SELEX round number and specie	Random region (N_{40})
152	9-4	ACUCGAACAUUUCCACUAACCAACCAUACUAAAGCACCGC
153	7-2	GACCACCAACACACCACAUACUGCUUUGUACCAACAUUC
154	6-1	CCCAGCGAACACACAACAGAACACGAACGGAUCCGAGCAA
155	6-2	GUCACAAACUACCUUCAUCCUUCGCUUGAUACAACAUUC
156	6-7	ACACCAAGGACCCAACGACCCUCGCUUGACACAGUCAUUC
157	6-8	AUGAACAACACCCAAACUUGCUUCAACCGCAUCCACA
158	6-11	GACCUCACGCACUGCUAAGCGGCUCUGAUGGAGCUCUAUG
159	6-13	CCACCUCCGAAAAAUCACAAUCUGCCCUUGACACCAGCUAG
160	6-17	CCUCAUUGGCCCUGCCACGCUCGGACAACCGUUCCGCUCA
161	6-21	UCCAGUGCAGUUCCAUAACCGCUACUCAGCGCGUGAUUAG
162	6-22	UUUCGAGCAACCUCCCAACAAUCUAACCGUAACCCUCCAG
163	6-27	CAACAUCAGCACGCCUGAACCUUCGCUUGCAACAGCAUUC
164	6-29	CCACCUCCGAAAAAUCACAAUCUGCCCUUGACACCAGCUAG
165	6-31	UUACACCAUCGACCAAACUAUGCGCCGUACCACUAUACGA

10

For Angiopoietin-2 (Ang2) Aptamers, a random library of 2'-fluoro modified RNA was created with the sequence: GGGAGGACGAUGCGG(SEQ ID NO:166)-N_{40}-CAGACGACUCGCUGAGGAUCCGAGA (SEQ ID NO:167).

15   *In vitro* selection was performed using recombinant human angiopoietin-2 (Ang2; R&D Systems, Minneapolis, Minnesota). To enhance the specificity of the Ang2 selection, molecules that bound the related agonist Angiopoietin-1* (Ang1*; Regeneron Pharmaceuticals) were discarded (negative selection) prior to rounds of positive selection for Ang2. After 11

rounds, the pool was cloned and sequenced, and a family of RNAs with a 12-nucleotide consensus region (italics) was identified and was represented by one dominant random region sequence (ANG11-1): ACUAGCCU*CAUCAGCUCAUG* UGCCCCUCCGCCUGGAUCAC (SEQ ID NO:168). As shown in Figure 27, direct binding (corrected fraction bound) of ANG11-1 RNA is plotted as a function of protein concentration. ANG11-1 binds Ang2 with a K_d of <10 nM and binds Ang1* with a K_d of ~1 µM (>100-fold specificity).

Table 8 sets forth additional representative Ang2 aptamers. Analysis of clones from rounds 9 and 11 revealed several unique random region sequences containing at least one of two conserved motifs, indicated by italics or underlining. Aptamer sequences are as follows: GGGAGGACGAUGCGG (SEQ ID NO:166) -N_{40}-CAGACGACUCGCUGAGGAUCCGAGA (SEQ ID NO:167).

Table 8

Ang2 Aptamers

SEQ ID NO:	Clone – SELEX round number and specie	Random region (N_{40})	Frequency	K_d
168	11-1	ACUAGCCU*CAUCAGCUCAUG*UGCCCCUCCGCCUGGAUCAC	10 of 26	~5 nM
169	11-2	UGACCAAGCCU<u>CACGUUGAAC</u>CUGCCAGUAGACCCCGCCCA	1 of 26	
170	11-3	UUAAC*CAUCAGCUCAUG*GCCCCUGCCCUCUCAAGGACCAC	1 of 26	~10 nM
171	11-4	CACCAGACCGAC*AUCAGCUUAUG*GCCCCUCACCCACACCG	1 of 26	
172	11-6	GGAGCGCAAUUCGCCUCGCAA<u>GUUGAACUC</u>CGCUGGCGG	1 of 26	
173	11-9	UA*AGCUC*UUUGGCUUAGCCCGACACGUUGAACUCCAGAGU	1 of 26	
174	11-10	CACGGUACCACCAAGUCA<u>CACGUUGAACUC</u>CAUGCAGCUG	1 of 26	
175	11-15	CCACCGAUCG*CAUCAGCUCAUG*GCCCCUCCCGACCCGCCA	1 of 26	
176	11-19	CCAG<u>ACGUU</u>CUCGCCCCGCCGAU*CAUCAGCGC*UGGCCCUAU	1 of 26	

177	11-26	CACUACCACGCCAU*AUCAGCU*AAUGGCCCCUCCCUACGCA	1 of 26	
178	11-30	CACUCAGCGCCCUGCGAA<u>ACGUUG</u>CCGCCUCCCAACGUCU	1 of 26	
179	11-32	ACUCACCAGUCACC*AUCAGCUC*AUGCGCCCCUCCCCCGAC	1 of 26	
180	11-34	CUCUUUUGUCCCCG<u>CACGUUGAACUC</u>CUGUCCCUCUACU	1 of 26	
181	11-36	UGACGGUUCUUCUCUCGCCUCUGG*AGCUC*UCGUCUCGAU	2 of 26	
182	9-1	CACUUU*AGCUC*ACGCCACCG<u>CACGUUGAAC</u>GCCCAUCCCG	1 of 8	
183	9-2	CAAUGCAG*CAUCAGCUC*AUGGCCCCUCCACAAGCGCGAAU	1 of 8	
184	9-3	CAUGUCUACAACAAUCUCGCCC<u>GUUGA</u>GUCUCGUCGAAUU	2 of 8	
185	9-5	CGAUCUUUUCGUCAACCG<u>CACGUUGAACUC</u>GGCUCGGCAC	1 of 8	~ 5 nM
186	9-6	CACCCGUCCGUCCAAAUCCGCUU<u>CGUUG</u>GACCCCAUCUU	1 of 8	

Referring now to Figure 30, application of sequence alignment and RNA-folding algorithms to the predominant sequence family suggests a common stem-looped structure that incorporated the conserved sequence motif. Shown is a truncated form (dubbed 11-1.41) of the above-noted aptamer 11.1 (SEQ ID NO:168). The sequence of 11-1.41 is GAGGACGAUGCGGACUAGCCUCAUCAGCUCAUGUGCCCUC (SEQ ID NO:187). Scrambling the 6-nucleotide consensus loop sequence (CAGCUC > ACUCCG) disrupts the ability of the truncate to bind Ang2 (K_d > 1000 nM), as does mutation of the sequence comprising the terminal stem ((K_d ~ 1000 nM).

II.G. General Considerations for Aptamers

When a consensus sequence is identified, oligonucleotides that contain that sequence can be made by conventional synthetic or recombinant techniques. These aptamers can also function as target-specific aptamers of this invention. Such an aptamer can conserve the entire nucleotide sequence of an isolated aptamer, or can contain one or more additions, deletions or substitutions in the nucleotide sequence, as long as a consensus sequence is conserved. A mixture of such aptamers can also function as target-specific aptamers, wherein the mixture is a set of aptamers with a portion or portions of their nucleotide sequence being random or varying, and a conserved region that contains the consensus sequence. Additionally, secondary aptamers can

be synthesized using one or more of the modified bases, sugars and linkages described herein using conventional techniques and those described herein.

In some embodiments of this invention, aptamers can be sequenced or mutagenized to identify consensus regions or domains that are participating in aptamer binding to target, and/or aptamer structure. This information is used for generating second and subsequent pools of aptamers of partially known or predetermined sequence. Sequencing used alone or in combination with the retention and selection processes of this invention, can be used to generate less diverse oligonucleotide pools from which aptamers can be made. Further selection according to these methods can be carried out to generate aptamers having preferred characteristics for diagnostic or therapeutic applications. That is, domains that facilitate, for example, drug delivery could be engineered into the aptamers selected according to this invention.

Although this invention is directed to making aptamers using screening from pools of non-predetermined sequences of oligonucleotides, it also can be used to make second-generation aptamers from pools of known or partially known sequences of oligonucleotides. A pool is considered diverse even if one or both ends of the oligonucleotides comprising it are not identical from one oligonucleotide pool member to another, or if one or both ends of the oligonucleotides comprising the pool are identical with non-identical intermediate regions from one pool member to another. Toward this objective, knowledge of the structure and organization of the target protein can be useful to distinguish features that are important for biochemical pathway inhibition or biological response generation in the first generation aptamers. Structural features can be considered in generating a second (less random) pool of oligonucleotides for generating second round aptamers.

Those skilled in the art will appreciate that comparisons of the complete or partial amino acid sequences of the purified protein target to identify variable and conserved regions is useful. Comparison of sequences of aptamers made according to this invention provides information about the consensus regions and consensus sequences responsible for binding. It is expected that certain nucleotides will be rigidly specified and certain positions will exclusively require certain bases. Likewise, studying localized regions of a protein to identify secondary structure can be useful. Localized regions of a

protein can adopt a number of different conformations including beta strands, alpha helices, turns (induced principally by proline or glycine residues) or random structure. Different regions of a polypeptide interact with each other through hydrophobic and electrostatic interactions and also by formation of

5   salt bridges, disulfide bridges, etc. to form the secondary and tertiary structures. Defined conformations can be formed within the protein organization, including beta sheets, beta barrels, and clusters of alpha helices.

It sometimes is possible to determine the shape of a protein target or

10   portion thereof by crystallography X ray diffraction or by other physical or chemical techniques known to those skilled in the art. Many different computer programs are available for predicting protein secondary and tertiary structure, the most common being those described in Chou, P. Y. and Fasman, G. D. (1978) *Biochemistry*, 13:222-245, and Garnier et al. (1978) J.

15   *Mol. Biol.*, 120:97-120. Generally, these and other available programs are based on the physical and chemical properties of individual amino acids (hydrophobicity, size, charge and presence of side chains) and on the amino acids' collective tendency to form identifiable structures in proteins whose secondary structure has been determined. Many programs attempt to weight

20   structural data with their known influences. For example, amino acids such as proline or glycine are often present where polypeptides have share turns. Long stretches of hydrophobic amino acids (as determined by hydropathy plot), usually have a strong affinity for lipids.

Data obtained by the methods described above and other conventional

25   methods and tools can be correlated with the presence of particular sequences of nucleotides in the first and second generation aptamers to engineer second and third generation aptamers. Further, according to this invention, second generation aptamers can be identified simply by sequentially screening from pools of oligonucleotides having more

30   predetermined sequences than the pools used in earlier rounds of selection.

These methods can be used to design optimal binding sequences for any desired protein target (which can be portions of aptamers or entire aptamers) and/or to engineer into aptamers any number of desired targeted functions or features. Optimal binding sequences will be those which exhibit

high relative affinity for target, i.e., affinity measured in K_d in at least in the nanomolar range, and, for certain drug applications, the nanomolar or picomolar range. In practicing this invention, studying the binding energies of aptamers using standard methods known generally in the art can be useful generally, consensus regions can be identified by comparing the conservation of nucleotides for appreciable enhancement in binding.

Structural knowledge can be used to engineer aptamers made according to this invention. For example, stem structures in the aptamer pool can be vital components in some embodiments where increased aptamer rigidity is desired. According to the teachings of the instant invention, a randomly generated pool of oligonucleotides having the stem sequences can be generated. After aptamers are identified which contain the stem (i.e., use the stem in primers), one can put cross-linkers in the stem to covalently fix the stem in the aptamer structure. Cross-linkers also can be used to fix an aptamer to a target.

Once an aptamer has been identified, it can be used, either by linkage to, or use in combination with, other aptamers identified according to these methods. One or more aptamers can be used in this manner to bind to one or more targets.

II.G.1. Techniques for Identifying Improved Nucleic Acid Ligands

In order to produce nucleic acids desirable for use as a pharmaceutical, it is preferred that the nucleic acid ligand binds to the target in a manner capable of achieving the desired effect on the target; be as small as possible to obtain the desired effect; be as stable as possible; and be a specific ligand to the chosen target. In most, if not all, situations it is preferred that the nucleic acid ligand has the highest possible affinity to the target. Modifications or derivatizations of the ligand that confer resistance to degradation and clearance *in situ* during therapy, the capability to cross various tissue or cell membrane barriers, or any other accessory properties that do not significantly interfere with affinity for the target molecule can also be provided as improvements.

One of the uses of nucleic acid ligands derived by SELEX or another approach is to find ligands that alter target molecule function. Thus, it is a

good procedure to first assay for inhibition or enhancement of function of the target protein. One could even perform such functional tests of the combined ligand pool prior to cloning and sequencing. Assays for the biological function of the chosen target are generally available and known to those skilled in the art, and can be easily performed in the presence of the nucleic acid ligand to determine if inhibition occurs.

Enrichment will supply a number of cloned ligands of probable variable affinity for the target molecule. Sequence comparisons can yield consensus secondary structures and primary sequences that allow grouping of the ligand sequences into motifs. Although a single ligand sequence (with some mutations) can be found frequently in the total population of cloned sequences, the degree of representation of a single ligand sequence in the cloned population of ligand sequences cannot absolutely correlate with affinity for the target molecule. Therefore mere abundance is not the sole criterion for judging "winners" after SELEX and binding assays for various ligand sequences (adequately defining each motif that is discovered by sequence analysis) are required to weigh the significance of the consensus arrived at by sequence comparisons. The combination of sequence comparison and affinity assays should guide the selection of candidates for more extensive ligand characterization.

An important avenue for narrowing down what amount of sequence is relevant to specific affinity is to establish the boundaries of that information within a ligand sequence. This is conveniently accomplished by selecting end-labeled fragments from hydrolyzed pools of the ligand of interest so that 5′ and 3′ boundaries of the information can be discovered. To determine a 3′ boundary, one can perform a large-scale *in vitro* transcription of the PCR'd ligand, gel purifies the RNA using UV shadowing on an intensifying screen, phosphatases the purified RNA, phenol extracts extensively, labels by kinasing with ^{32}P, and gel purifies the labeled product (using a film of the gel as a guide). The resultant product can then be subjected to pilot partial digestions with RNase T1 (varying enzyme concentration and time, at 50°C. in a buffer of 7M urea, 50 mM sodium citrate pH 5.2) and alkaline hydrolysis (at 50 mM $NaCO_3$, adjusted to pH 9.0 by prior mixing of 1M bicarbonate and carbonate solutions; test over ranges of 20 to 60 minutes at 95°C). Once

optimal conditions for alkaline hydrolysis are established (so that there is an even distribution of small to larger fragments) one can scale up to provide enough material for selection by the target (usually on nitrocellulose filters).

5   One then sets up binding assays, varying target protein concentration from the lowest saturating protein concentration to that protein concentration at which approximately 10% of RNA is bound as determined by the binding assays for the ligand. One should vary target concentration (if target supplies allow) by increasing volume rather than decreasing absolute amount of target; this provides a good signal to noise ratio as the amount of RNA bound to the

10   filter is limited by the absolute amount of target. The RNA is eluted as, for example, in SELEX and then run on a denaturing gel with T1 partial digests so that the positions of hydrolysis bands can be related to the ligand sequence.

The 5′ boundary can be similarly determined. Large-scale *in vitro*

15   transcriptions are purified as described above. There are two methods for labeling the 3′ end of the RNA. One method is to kinase Cp with ^{32}P (or purchase ^{32}P-Cp) and ligate to the purified RNA with RNA ligase. The labeled RNA is then purified as above and subjected to very identical protocols. An alternative is to subject unlabeled RNAs to partial alkaline hydrolyses and

20   extend an annealed, labeled primer with reverse transcriptase as the assay for band positions. One of the advantages over pCp labeling is the ease of the procedure, the more complete sequencing ladder (by dideoxy chain termination sequencing) with which one can correlate the boundary, and increased yield of assayable product. A disadvantage is that the extension on

25   eluted RNA sometimes contains artifactual stops, so it can be important to control by spotting and eluting starting material on nitrocellulose filters without washes and assaying as the input RNA.

The result is that it is possible to find the boundaries of the sequence information required for high affinity binding to the target.

30

II.G.2. Assessment of Nucleotide Contributions to Affinity

Once a minimal high affinity ligand sequence is identified, it can be useful to identify the nucleotides within the boundaries that are crucial to the interaction with the target molecule. One method is to create a new random

template in which all of the nucleotides of a high affinity ligand sequence are partially randomized or blocks of randomness are interspersed with blocks of complete randomness for use in a SELEX method for example, preferably a modified or toggle SELEX method as disclosed herein. Such "secondary"

5   SELEXes produce a pool of ligand sequences in which crucial nucleotides or structures are absolutely conserved, less crucial features preferred, and unimportant positions unbiased. Secondary SELEXes can thus help to further elaborate a consensus that is based on relatively few ligand sequences. In addition, even higher-affinity ligands can be provided whose sequences were

10   unexplored in the original SELEX.

Another method is to test oligo-transcribed variants (i.e. nucleotide substituion) where the consensus sequence can be unclear.

Another useful set of techniques are inclusively described as chemical modification experiments. Such experiments can be used to probe the native

15   structure of RNAs, by comparing modification patterns of denatured and non-denatured states. The chemical modification pattern of an RNA ligand that is subsequently bound by target molecule can be different from the native pattern, indicating potential changes in structure upon binding or protection of groups by the target molecule. In addition, RNA ligands will fail to be bound by

20   the target molecule when modified at positions crucial to either the bound structure of the ligand or crucial to interaction with the target molecule. Such experiments in which these positions are identified are described as "chemical modification interference" experiments.

There are a variety of available reagents to conduct such experiments

25   that are known to those skilled in the art (see, Ehresmann et al., *Nuc. Acids. Res.*, 15:9109-9128, (1987)). Chemicals that modify bases can be used to modify ligand RNAs. A pool is bound to the target at varying concentrations and the bound RNAs recovered (much as in the boundary experiments) and the eluted RNAs analyzed for the modification. An assay can be by

30   subsequent modification-dependent base removal and aniline scission at the baseless position or by reverse transcription assay of sensitive (modified) positions. In such assays bands (indicating modified bases) in unselected RNAs appear that disappear relative to other bands in target protein-selected RNAs. Similar chemical modifications with ethylnitrosourea, or via mixed

chemical or enzymatic synthesis with, for example, 2′-methoxys on ribose or phosphorothioates can be used to identify essential atomic groups on the backbone. In experiments with 2′-methoxy vs. 2′-OH mixtures, the presence of an essential OH group results in enhanced hydrolysis relative to other

5   positions in molecules that have been stringently selected by the target.

Comparisons of the intensity of bands for bound and unbound ligands can reveal not only modifications that interfere with binding, but also modifications that enhance binding. A ligand can be made with precisely that modification and tested for the enhanced affinity. Thus chemical modification

10   experiments can be a method for exploring additional local contacts with the target molecule, just as "walking" (see below) is for additional nucleotide level contacts with adjacent domains.

A consensus of primary and secondary structures that enables the chemical or enzymatic synthesis of oligonucleotide ligands whose design is

15   based on that consensus is provided herein via a SELEX method, preferably a modified or toggle SELEX method as disclosed herein. Because the replication machinery of SELEX requires that rather limited variation at the subunit level (ribonucleotides, for example), such ligands imperfectly fill the available atomic space of a target molecule's binding surface. However, these

20   ligands can be thought of as high-affinity scaffolds that can be derivatized to make additional contacts with the target molecule. In addition, the consensus contains atomic group descriptors that are pertinent to binding and atomic group descriptors that are coincidental to the pertinent atomic group interactions. Such derivatization does not exclude incorporation of cross-

25   linking agents that will give specifically directly covalent linkages to the target protein. Such derivatization analyses can be performed at but are not limited to the 2′ position of the ribose, and thus can also include derivatization at any position in the base or backbone of the nucleotide ligand.

The present invention thus includes nucleic acid ligands wherein

30   certain chemical modifications have been made in order to increase the *in vivo* stability of the ligand or to enhance or mediate the delivery of the ligand. Examples of such modifications include chemical substitutions at the ribose and/or phosphate positions of a given RNA sequence. See, e.g., Cook et al., PCT Application WO 9203568; U.S. Pat. No. 5,118,672 to Schinazi et al.;

Hobbs et al., *Biochem* 12:5138 (1973); Guschlbauer et al., *Nucleic Acids Res.* 4:1933 (1977); Shibahara et al., *Nucl. Acids. Res.* 15:4403 (1987); Pieken et al., *Science* 253:314 (1991), each of which is specifically incorporated herein by reference.

A logical extension of this analysis is a situation in which one or a few nucleotides of the polymeric ligand is used as a site for chemical derivative exploration. The rest of the ligand serves to anchor in place this monomer (or monomers) on which a variety of derivatives are tested for non-interference with binding and for enhanced affinity. Such explorations can result in small molecules that mimic the structure of the initial ligand framework, and have significant and specific affinity for the target molecule independent of that nucleic acid framework. Such derivatized subunits, which can have advantages with respect to mass production, therapeutic routes of administration, delivery, clearance or degradation than the initial ligand, can become the therapeutic and can retain very little of the original ligand. Thus, the aptamer ligands of the present invention can allow directed chemical exploration of a defined site on the target molecule known to be important for the target function.

II.F.3. Walking Experiments

After a minimal consensus ligand sequence has been determined for a given target, it is possible to add random sequence to the minimal consensus ligand sequence and evolve additional contacts with the target, perhaps to separate but adjacent domains. This procedure has been referred to in the art as "walking".

A walking experiment can involve two experiments performed sequentially. A new candidate mixture is produced in which each of the members of the candidate mixture has a fixed nucleic acid region that corresponds to a nucleic acid ligand of interest. Each member of the candidate mixture also contains a randomized region of sequences. According to this method it is possible to identify what are referred to as "extended" nucleic acid ligands, which contain regions that can bind to more than one binding domain of a target.

II.F.4. Covariance Analysis

In conjunction with empirical methods for determining the three dimensional structure of nucleic acids, computer modeling methods for determining structure of nucleic acid ligands can also be employed.

Secondary structure prediction is a useful guide to correct sequence alignment. It is also a highly useful stepping-stone to correct 3D structure prediction, by constraining a number of bases into A-form helical geometry.

Tables of energy parameters for calculating the stability of secondary structures exist. Although early secondary structure prediction programs attempted to simply maximize the number of base-pairs formed by a sequence, most current programs seek to find structures with minimal free energy as calculated by these thermodynamic parameters. There are two problems in this approach that should be borne in mind. First, the thermodynamic rules are inherently inaccurate, typically to 10% or so, and there are many different possible structures lying within 10% of the global energy minimum. Second, the actual secondary structure need not lie at a global energy minimum, depending on the kinetics of folding and synthesis of the sequence. Nonetheless, for short sequences, these caveats are of minor importance because there are so few possible structures that can form.

The brute force predictive method is a dot-plot: make an N by N plot of the sequence against itself, and mark an X everywhere a base pair is possible. Diagonal runs of X's mark the location of possible helices. Exhaustive tree-searching methods can then search for all possible arrangements of compatible (i.e., non-overlapping) helices of length L or more; energy calculations can be done for these structures to rank them as more or less likely. The advantages of this method are that all possible topologies, including pseudoknotted conformations, can be examined, and that a number of suboptimal structures are automatically generated as well. The disadvantages of the method are that it can run in the worst cases in time proportional to an exponential factor of the sequence size, and cannot (depending on the size of the sequence and the actual tree search method employed) look deep enough to find a global minimum.

An elegant predictive method, and currently the most used, is the Zuker program. Zuker (1989) *Science* 244:48-52. Originally based on an

algorithm developed by Ruth Nussinov, the Zuker program makes a major simplifying assumption that no pseudoknotted conformations will be allowed. This permits the use of a dynamic programming approach that runs in time proportional to only N3 to N4, where N is the length of the sequence. The

5   Zuker program is the only program capable of rigorously dealing with sequences of than a few hundred nucleotides, so it has come to be the most commonly used by biologists. However, the inability of the Zuker program to predict pseudoknotted conformations is a serious consideration. Where pseudoknotted RNA structures are suspected or are recognized by eye, a

10   brute-force method capable of predicting pseudoknotted conformations should be employed.

        A central element of comparative sequence analysis is sequence covariations. A covariation is when the identity of one position depends on the identity of another position; for instance, a required Watson-Crick base pair

15   shows strong covariation in that knowledge of one of the two positions gives absolute knowledge of the identity at the other position. Covariation analysis has been used previously to predict the secondary structure of RNAs for which a number of related sequences sharing a common structure exist, such as tRNA, rRNAs, and group I introns. It is now apparent that covariation

20   analysis can be used to detect tertiary contacts as well.

        Stormo and Gutell (1992) *Nucleic Acids Research* 29:5785-5795 have designed and implemented an algorithm that precisely measures the amount of covariations between two positions in an aligned sequence set. The program is called "MIXY"-Mutual Information at position X and Y. Consider an

25   aligned sequence set. In each column or position, the frequency of occurrence of A, C, G, U, and gaps is calculated. Call this frequency $f(bx)$, the frequency of base b in column x. Now consider two columns at once. The frequency that a given base b appears in column x is $f(bx)$ and the frequency that a given base b appears in column y is $f(by)$. If position x and position y do

30   not care about each other's identity-that is, the positions are independent; there is no covariation-the frequency of observing bases bx and by at position x and y in any given sequence should be just $f(bxby)=f(bx)f(by)$. If there are substantial deviations of the observed frequencies of pairs from their expected frequencies, the positions are said to covary.

The amount of deviation from expectation can be quantified with an information measure M(x,y), the mutual information of x and y:

$$M(x,\ y) = \sum_{b_x b_y} f(b_x b_y) ln \frac{f(b_x b_y)}{f(b_x) f(b_y)}$$

5   M(x,y) can be described as the number of bits of information one learns about the identity of position y from knowing just the identity of position y from knowing just the identity of position x. If there is no covariation, M(x,y) is zero; larger values of M(x,y) indicate strong covariation. Covariation values can be used to develop three-dimensional structural predictions.

10   In some ways, the problem is similar to that of structure determination by NMR. Unlike crystallography, which in the end yields an actual electron density map, NMR yields a set of interatomic distances. Depending on the number of interatomic distances one can get, there can be one, few, or many 3D structures with which they are consistent. Mathematical techniques had to

15   be developed to transform a matrix of interatomic distances into a structure in 3D space. The two main techniques in use are distance geometry and restrained molecular dynamics.

Distance geometry is the more formal and purely mathematical technique. The interatomic distances are considered to be coordinates in an

20   N-dimensional space, where N is the number of atoms. In other words, the "position" of an atom is specified by N distances to all the other atoms, instead of the three (x,y,z) coordinates typically considered. Interatomic distances between every atom are recorded in an N-by-N distance matrix. A complete and precise distance matrix is easily transformed into a 3 by N

25   Cartesian coordinates, using matrix algebra operations. The trick of distance geometry as applied to NMR is dealing with incomplete (only some of the interatomic distances are known) and imprecise data (distances are known to a precision of only a few angstroms at best). Much of the time of distance geometry-based structure calculation is thus spent in pre-processing the

30   distance matrix, calculating bounds for the unknown distance values based on the known ones, and narrowing the bounds on the known ones. Usually,

multiple structures are extracted from the distance matrix that are consistent with a set of NMR data; if they all overlap nicely, the data were sufficient to determine a unique structure. Unlike NMR structure determination, covariance gives only imprecise distance values, but also only probabilistic rather than absolute knowledge about whether a given distance constraint should be applied.

Restrained molecular dynamics can also be employed, albeit in a more ad hoc manner. Given an empirical force field that attempts to describe the forces that all the atoms feel (van der Waals, covalent bonding lengths and angles, electrostatics), one can simulate a number of femtosecond time steps of a molecule's motion, by assigning every atom at a random velocity (from the Boltzmann distribution at a given temperature) and calculating each atom's motion for a femtosecond using Newtonian dynamical equations; that is "molecular dynamics". In restrained molecular dynamics, one assigns extra ad hoc forces to the atoms when they violate specified distance bounds.

With respect to RNA aptamers, the probabilistic nature of data with restrained molecular dynamics can be addressed. The covariation values can be transformed into artificial restraining forces between certain atoms for certain distance bounds; varying the magnitude of the force according to the magnitude of the covariance.

NMR and covariance analysis generates distance restraints between atoms or positions, which are readily transformed into structures through distance geometry or restrained molecular dynamics. Another source of experimental data which can be utilized to determine the three dimensional structures of nucleic acids is chemical and enzymatic protection experiments, which generate solvent accessibility restraints for individual atoms or positions.

II.H. Utility of the Aptamers

The aptamers and modified aptamers of the invention are useful in diagnostic, research and therapeutic contexts. For diagnostic applications, aptamers are particularly well suited for binding to biomolecules that are identical or similar between different species. Classes of molecules such as coagulation factors and transcription factors generally do not serve as good

antigens because they are not easily recognized as foreign by the immune systems of animals that can be used to generate antibodies. Antibodies are generally used to bind analytes that are detected or quantitated in various diagnostic assays. Aptamers represent a class of molecules that can be used

5   in place of antibodies for diagnostic and purification purposes.

The aptamers of the invention are therefore particularly useful as diagnostic reagents to detect the presence or absence of the target substances to which they specifically bind. Such diagnostic tests are conducted by contacting a sample with the specifically binding oligonucleotide

10   to obtain a complex that is then detected by conventional techniques. For example, the aptamers can be labeled using radioactive, fluorescent, or chromogenic labels and the presence of label bound to solid support to which the target substance has been bound through a specific or nonspecific binding means detected. Alternatively, the specifically binding aptamers can be used

15   to effect initial complexation to the support. Techniques for conducting assays using such oligomers as specific binding partners are generally known to track those for standard specific binding partner based assays.

This invention also permits the recovery and deduction of oligomeric sequences that bind specifically to target proteins and specific portions

20   thereof. Therefore, these oligonucleotides can be used as a separation tool for retrieving the substances to which they specifically bind. By coupling the oligonucleotides containing the specifically binding sequences to a solid support, for example, proteins or other cellular components to which they bind can be recovered in useful quantities. In addition, these oligonucleotides can

25   be used in diagnosis by employing them in specific binding assays for the target substances. When suitably labeled using detectable moieties such as radioisotopes, the specifically binding oligonucleotides can also be used for *in vivo* imaging or histological analysis.

It can be commented that the mechanism by which the specifically

30   binding oligomers of the invention interfere with or inhibit the activity of a target substance is not always established, and is not a part of the invention. The oligomers of the invention are characterized by their ability to target specific substances regardless of the mechanisms of targeting or the mechanism of the effect thereof.

For use in research, the specifically binding oligonucleotides of the invention are especially helpful in effecting the isolation and purification of substances to which they bind. For this application, typically, the oligonucleotide containing the specific binding sequences is conjugated to a solid support and used as an affinity ligand in chromatographic separation of the target substance. The affinity ligand can also be used to recover previously unknown substances from sources that do not contain the target substance by virtue of binding similarity between the intended target and the unknown substances. Furthermore, as data accumulate with respect to the nature of the nonoligonucleotide/oligonucleotide-specific binding, insight can be gained as to the mechanisms for control of gene expression.

The aptamers described herein can be used as a separation reagent for retrieving the targets to which they specifically bind. By coupling the oligonucleotides containing the specifically binding sequences to a solid support, for example, the target substances can be recovered in useful quantities. In addition, these oligonucleotides can be used in diagnosis by employing them in specific binding assays for the target substances. When suitably labeled using detectable moieties including radioisotopes such as ^{19}F, ^{99m}Tc, ^{131}I, ^{90}Y, ^{111}In, ^{123}I, ^{15}N, ^{32}P or ^{33}P, the specifically binding oligonucleotides can also be used for in vivo or in vitro diagnosis, imaging or histological analysis by techniques known in the art.

For application in such various uses, the aptamers of the invention can be coupled to auxiliary substances that enhance or complement the function of the aptamer. Such auxiliary substances include, for example, labels such as radioisotopes, fluorescent labels, enzyme labels and the like; specific binding reagents such as antibodies, additional aptamer sequence, cell surface receptor ligands, receptors per se and the like; toxins such as diphtheria toxin, tetanus toxin or ricin; drugs such as antiinflammatory, antibiotic, or metabolic regulator pharmaceuticals, solid supports such as chromatographic or electrophoretic supports, and the like. Suitable techniques for coupling of aptamers to desired auxiliary substances are generally known for a variety of such auxiliary substances, and the specific nature of the coupling procedure will depend on the nature of the auxiliary substance chosen. Coupling can be direct covalent coupling or can involve the use of

synthetic linkers such as those marketed by Pierce Chemical Co., Rockford, Illinois.

Thus, the aptamers or modified aptamers of the invention can be used alone in therapeutic applications or can be used as targeting agents to deliver
5 pharmaceuticals or toxins to desired targets. The aptamers can be used in diagnostic procedures and advantageously in this application include label. They can be used as reagents to separate target molecules from contaminants in samples containing the target molecules in which application they are advantageously coupled to solid support.

10

III. Synthesis of RNA Aptamers

In a representative embodiment of the present invention, an RNA aptamer is synthesized on a solid support column, using conventional techniques such as those described by Beaucage et al. (1981) *Tetrahedr.*
15 *Letters* 22:1859-1862 and Sinha et al., (1984) *Nucleosides and Nucleotides* 3:157-171, both of which are incorporated by reference. The final DMT-group is removed from the resulting RNA aptamer. Alternately, if large-scale synthesis is used, the RNA aptamer can be made by scale-up of the solid support method or the RNA aptamer can be made by using solution phase
20 techniques, particularly if the desired end-product is a relatively short oligonucleotide. A starting material for the synthesis process can be a 5'-non-tritylated RNA oligoribo-nucleotide or analog of the desired primary structure, which preferably can have protected bases, and which is preferably bound to a solid-support. Any conventionally used protecting groups can be used.
25 Typically N_6 -benzoyl is used for adenine, N_4 -benzoyl for cytosine, N_2 - isobutyryl for guanine and N_2 -benzoyl for 2-amino purine. Other useful protecting groups include phenoxyacetyl (PAC) and t-butoxyacetyl (TAC). Conveniently, the more base labile protection groups should be used for the synthesis of the RNA or analog fragment; those of ordinary skill in the art
30 know these groups. Such groups can help to prevent hydrolysis of the generated tri- or diphosphates, which are generally quite stable under basic conditions, but could be subject to some hydrolysis. Other envisioned modifications are disclosed in U.S. Patent No. 6,011,020, incorporated herein by reference, and include but are not limited to the incorporation of

bioavailability enhancing molecules such as PEG or cholesterol via a covalent linkage.

A capped RNA or analog of this invention can be of any length, the only limit being that of the synthesis technique employed to prepare the RNA or analog. Currently, a preferred length is ranges from approximately 15 to 100 bases, but with improvements in synthetic technology the length of the oligonucleotide is expected to increase. For purposes of this invention, it is preferred that the capped RNA or analog be less than approximately 100 bases in length, and preferably less than about 40 bases in length.

In addition, nucleoside analogs such as 2'-deoxy, 2'-halo, 2'-amino (not substituted or mono- or disubstituted), 2'-mono, di- or trihalomethyl, 2'-O-alkyl, 2'-O-halo-substituted alkyl, 2'-alkyl, azido, phosphorothioate, sulfhydryl, methylphosphonate, fluorescein, rhodamine, pyrene, biotin, xanthine, hypoxanthine, 2,6-diamino purine, 2-hydroxy-6-mercaptopurine and pyrimidine bases substituted at the 6-position with sulfur or 5 position with halo or C_{1-5} alkyl groups, abasic linkers, 3'-deoxy-adenosine as well as other available "chain terminator" or "non-extendible" analogs (at the 3'-end of the RNA), and the like can be incorporated during the RNA synthesis. Further, various labels such as ^{32}P or ^{33}P and the like can likewise be incorporated during the synthesis, resulting in novel RNA analogs produced by this process. Other envisioned modifications are disclosed in U.S. Patent No. 6,011,020, incorporated herein by reference, and include but are not limited to the incorporation of 3' caps, such an inverted DT cap, or an inverted abasic cap, or combination thereof.

IV. Therapeutic Methods

A method of modulating the biological activity of a coagulation pathway factor is provided in accordance with the present invention. In a preferred embodiment, the method comprises: (a) administering to a warm blooded vertebrate in need thereof an effective amount of an RNA aptamer that selectively binds a coagulation pathway factor, the RNA aptamer having a dissociation constant for the coagulation pathway factor of about 20 nM or less; and (b) modulating the biological activity of the coagulation pathway factor in the warm-blooded vertebrate through the administering of the RNA

aptamer in step (a).

A method of treating cardiovascular disease in a warm-blooded vertebrate is also provided in accordance with the present invention. The method comprises administering an effective amount of an RNA aptamer that selectively binds a coagulation pathway factor, the RNA aptamer having a dissociation constant for the coagulation pathway factor of about 20 nM or less, to a vertebrate subject suffering from cardiovascular disease, whereby cardiovascular disease in the vertebrate subject is treated.

A method of modulating E2F activity in a warm-blooded vertebrate in which such modulation is desired is also provided. The method comprises: (a) administering to the warm-blooded vertebrate an effective amount of an RNA aptamer that selectively binds an E2F family member, the RNA aptamer having a dissociation constant for the E2F family member of about 20 nM or less; and (b) modulating E2F in the warm-blooded vertebrate through the administering of the RNA aptamer of step (a).

The patient treated in the present invention in its many embodiments is desirably a human patient, although it is to be understood that the principles of the invention indicate that the invention is effective with respect to all vertebrate species, including warm-blood vertebrates (e.g. birds and mammals), which are intended to be included in the term "patient". In this context, a mammal is understood to include any mammalian species in which treatment of cardiovascular disease is desirable, particularly agricultural and domestic mammalian species.

Contemplated is the treatment of mammals such as humans, as well as those mammals of importance due to being endangered (such as Siberian tigers), of economical importance (animals raised on farms for consumption by humans and/or social importance (animals kept as pets or in zoos) to humans, for instance, carnivores other than humans such as cats and dogs), swine (pigs, hogs, and wild board), ruminants (such as cattle, oxen, sheep, giraffes, deer goats, bison, and camels), and horses. Also contemplated is the treatment of birds, including the treatment of those kinds of birds that are endangered, kept in zoos, as well as fowl, and more particularly domesticated fowl, i.e., poultry, such as turkeys, chickens, ducks, geese, guinea fowl, and the like, as they are also of economical importance to humans.

The present method for treating cardiovascular disease in a tissue contemplates contacting a tissue in which cardiovascular disease is occurring, or is at risk for occurring, with a composition comprising a therapeutically effective amount of an RNA aptamer capable of binding a coagulation factor.

5   Thus, the method comprises administering to a patient a therapeutically effective amount of a physiologically tolerable composition containing the RNA aptamer.

The dosage ranges for the administration of the RNA aptamer depend upon the form of the modulator, and its potency, as described further herein,

10   and are amounts large enough to produce the desired effect in which coagulation is modulated, which can correspondingly ameliorate cardiovascular disease and the symptoms of cardiovascular disease. The dosage should not be so large as to cause adverse side effects, such as hyperviscosity syndromes, pulmonary edema, congestive heart failure, and

15   the like. Generally, the dosage will vary with the age, condition, sex and extent of the disease in the patient and can be determined by one of skill in the art. The individual physician in the event of any complication can also adjust the dosage.

A therapeutically effective amount is an amount of an RNA aptamer

20   sufficient to produce a measurable modulation of coagulation in the tissue being treated, i.e., a coagulation-modulating amount, an E2F activity-modulating amount coagulation, and/or angiogenesis factor activity (e.g. Ang1 or Ang2 activity)-modulating amount. Modulation of coagulation, E2F activity, and/or angiogenesis factor activity (e.g. Ang1 or Ang2 activity) can be

25   measured *in situ* by immunohistochemistry by methods disclosed in the Laboratory Examples, or by other methods known to one skilled in the art. By the term "modulate" and grammatical variations thereof, it is intended an increase, decrease, or other alteration of any or all biological activities or properties a target.

30   Insofar as a coagulation modulator, E2F modulator, or angiogenesis factor activity (e.g. Ang1 or Ang2 activity) modulator can take the form of RNA aptamers it is to be appreciated that the potency, and therefore an expression of a "therapeutically effective" amount can vary. However, as shown by the

methods presented in the Laboratory Examples, one skilled in the art can readily assess the potency of a candidate RNA aptamer of this invention.

A preferred RNA aptamer has the ability to substantially bind to a target in solution at modulator concentrations of less than one (1) micromolar (µM), preferably less than 0.1 µM, and more preferably less than 0.01 µM. By "substantially" is meant that at least a 50 percent reduction in target biological activity is observed by modulation in the presence of the a target, and at 50% reduction is referred to herein as an IC_{50} value.

The RNA aptamers of the present invention can be administered parenterally by injection or by gradual infusion over time. Although the tissue to be treated can typically be accessed in the body by systemic administration and therefore most often treated by intravenous administration of therapeutic compositions, other tissues and delivery techniques are provided where there is a likelihood that the tissue targeted contains the target molecule. Thus, an RNA aptamer of the present invention can be administered orally, topically to a vascular tissue, intravenously, intraperitoneally, intramuscularly, subcutaneously, intra-cavity, transdermally, and can be delivered by peristaltic techniques. Representative, non-limiting approaches for topical administration to a vascular tissue include (1) coating or impregnating a blood vessel tissue with a gel comprising an aptamer of the present invention, for delivery *in vivo*, e.g. by implanting the coated or impregnated vessel in place of a damaged or diseased vessel tissue segment that was removed or by-passed; (2) delivery via a catheter to a vessel in which delivery is desired; and (3) pumping an aptamer composition of the present invention into a vessel that is to be implanted into a patient.

The therapeutic compositions comprising an RNA aptamer polypeptide of the present invention are conventionally administered intravenously, as by injection of a unit dose, for example. The term "unit dose" when used in reference to a therapeutic composition of the present invention refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent; i.e., carrier or vehicle.

The compositions are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered depends on the subject to be treated, capacity of the subject's system to utilize the active ingredient, and degree of therapeutic effect desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are peculiar to each individual. However, suitable dosage ranges for systemic application are disclosed herein and depend on the route of administration. Suitable regimes for administration are also variable, but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other administration. Alternatively, continuous intravenous infusion sufficient to maintain concentrations in the blood in the ranges specified for *in vivo* therapies are contemplated.

The present invention contemplates therapeutic compositions useful for practicing the therapeutic methods described herein. Therapeutic compositions of the present invention contain a physiologically tolerable carrier together with an RNA aptamer as described herein, dissolved or dispersed therein as an active ingredient. In a preferred embodiment, the therapeutic composition is not immunogenic when administered to a subject for therapeutic purposes.

As used herein, the terms "pharmaceutically acceptable", "physiologically tolerable" and grammatical variations thereof, as they refer to compositions, carriers, diluents and reagents, are used interchangeably and represent that the materials are capable of administration to or upon a patient without the production of undesirable physiological effects such as nausea, dizziness, gastric upset and the like.

Pharmaceutically useful compositions comprising an RNA aptamer of the present invention can be formulated according to known methods such as by the admixture of a pharmaceutically acceptable carrier. Examples of such carriers and methods of formulation can be found in *Remington's Pharmaceutical Sciences*. To form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of the aptamer. Such compositions can contain admixtures of more than one aptamer.

Therapeutic or prophylactic compositions of the invention are administered to an individual in amounts sufficient to modulate coagulation and/or to treat or prevent cardiovascular disease. The effective amount can vary according to a variety of factors such as the individual's condition, weight,

5   sex and age. Other factors include the mode of administration. Generally, the compositions will be administered in dosages adjusted for body weight, e.g. dosages ranging from about 1 μg/kg body weight to about 1 mg/kg body weight.

As noted above, the pharmaceutical compositions can be provided to

10   the individual by a variety of routes such orally, topically to a vascular tissue, intravenously, intraperitoneally, intramuscularly, subcutaneously, intra-cavity, transdermally, and can be delivered by peristaltic techniques. Representative, non-limiting approaches for topical administration to a vascular tissue include (1) coating or impregnating a blood vessel tissue with

15   a gel comprising an aptamer of the present invention, for delivery *in vivo*, e.g. by implanting the coated or impregnated vessel in place of a damaged or diseased vessel tissue segment that was removed or by-passed; (2) delivery via a catheter to a vessel in which delivery is desired; and (3) pumping an aptamer composition of the present invention into a vessel that is to be

20   implanted into a patient. Alternatively, the aptamer can be introduced into cells by microinjection, or by liposome encapsulation. Advantageously, aptamers of the present invention can be administered in a single daily dose, or the total daily dosage can be administered in several divided doses.

Aptamers can be particularly useful for the treatment of diseases where

25   it is beneficial to inhibit coagulation, E2F activity, and/or angiogenesis factor activity (e.g. Ang1 or Ang2 activity), or prevent such activity from occurring. The pharmaceutical compositions are administered in therapeutically effective amounts, that is, in amounts sufficient to generate a coagulation-, E2F activity-, and/or angiogenesis factor activity (e.g. Ang1 or Ang2 activity)-

30   modulating response, or in prophylactically effective amounts, that is in amounts sufficient to prevent a coagulation factor from acting in a coagulation cascade, to prevent an E2F activity-mediated response, or to prevent an angiogenesis factor activity (e.g. Ang1 or Ang2 activity)-mediated response.

The therapeutically effective amount and prophylactically effective amount can vary according to the type of aptamer. The pharmaceutical composition can be administered in single or multiple doses.

Aptamers synthesized or identified according to the methods disclosed herein can be used alone at appropriate dosages defined by routine testing in order to obtain optimal modulation of coagulation, E2F activity, and/or angiogenesis factor activity (e.g. Ang1 or Ang2 activity) while minimizing any potential toxicity. In addition, co-administration or sequential administration of other agents can be desirable. For combination treatment with more than one active agent, where the active agents are in separate dosage formulations, the active agents can be administered concurrently, or they each can be administered at separately staggered times.

The dosage regimen utilizing the aptamers of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal and hepatic function of the patient; and the particular aptamer employed. A physician of ordinary skill can readily determine and prescribe the effective amount of the aptamer required to prevent, counter or arrest the progress of the condition. Optimal precision in achieving concentrations of aptamer within the range that yields efficacy without toxicity requires a regimen based on the kinetics of the aptamer's availability to target sites. This involves a consideration of the distribution, equilibrium, and elimination of the aptamer.

In the methods of the present invention, the aptamers herein described in detail can form the active ingredient, and are typically administered in admixture with suitable pharmaceutical diluents, excipients or carriers (collectively referred to herein as "carrier" materials) suitably selected with respect to the intended form of administration, that is, oral tablets, capsules, elixirs, syrup, suppositories, gels and the like, and consistent with conventional pharmaceutical practices.

For instance, for oral administration in the form of a tablet or capsule, the active drug component can be combined with an oral, non-toxic pharmaceutically acceptable inert carrier such as ethanol, glycerol, water and the like. Moreover, when desired or necessary, suitable binders, lubricants,

disintegrating agents and coloring agents can also be incorporated into the mixture. Suitable binders include without limitation, starch, gelatin, natural sugars such as glucose or beta-lactose, corn sweeteners, natural and synthetic gums such as acacia, tragacanth or sodium alginate,

5 carboxymethylcellulose, polyethylene glycol, waxes and the like. Lubricants used in these dosage forms include, without limitation, sodium oleate, sodium stearate, magnesium stearate, sodium benzoate, sodium acetate, sodium chloride and the like. Disintegrators include, without limitation, starch, methyl cellulose, agar, bentonite, xanthan gum and the like.

10 For liquid forms the active drug component can be combined in suitably flavored suspending or dispersing agents such as the synthetic and natural gums, for example, tragacanth, acacia, methyl-cellulose and the like. Other dispersing agents that can be employed include glycerin and the like. For parenteral administration, sterile suspensions and solutions are desired.

15 Isotonic preparations that generally contain suitable preservatives are employed when intravenous administration is desired.

Topical preparations containing the active drug component can be admixed with a variety of carrier materials well known in the art, such as, e.g., alcohols, aloe vera gel, allantoin, glycerine, vitamin A and E oils, mineral oil,

20 PPG2 myristyl propionate, and the like, to form, e.g., alcoholic solutions, topical cleansers, cleansing creams, skin gels, skin lotions, and shampoos in cream or gel formulations.

The compounds of the present invention can also be administered in the form of liposome delivery systems, such as small unilamellar vesicles,

25 large unilamellar vesicles and multilamellar vesicles. Liposomes can be formed from a variety of phospholipids, such as cholesterol, stearylamine or phosphatidylcholines.

The compounds of the present invention can also be coupled with soluble polymers as targetable drug carriers. Such polymers can include

30 polyvinyl-pyrrolidone, pyran copolymer, polyhydroxypropylmethacryl-amidephenol, polyhydroxy-ethylaspartamidephenol, or polyethyl-eneoxidepolylysine substituted with palmitoyl residues. Furthermore, the compounds of the present invention can be coupled (preferably via a covalent linkage) to a class of biodegradable polymers useful in achieving controlled

release of a drug, for example, polyethylene glycol (PEG), polylactic acid, polyepsilon caprolactone, polyhydroxy butyric acid, polyorthoesters, polyacetals, polydihydro-pyrans, polycyanoacrylates and cross-linked or amphipathic block copolymers of hydrogels. Cholesterol and similar molecules can be linked to the aptamers to increase and prolong bioavailability.

V.   Methods of Identifying Aptamers

A method of identifying a ligand to a target from a candidate mixture of potential ligands is also provided in accordance with the present invention. Products, i.e. ligands, produced or identified by a method of the present invention are also provided.

In one embodiment the method preferably comprises: (a) preparing a candidate mixture of potential ligands; (b) contacting the candidate mixture with a target substrate in a lower stringency buffer, wherein ligands having increased affinity to the target relative to the candidate mixture bind to the target; (c) removing unbound candidate mixture; and (d) collecting the ligands that are bound to the target to produce a first collected ligand mixture. More preferably, the method further comprises: (e) contacting the first collected ligand mixture with the target in a higher stringency buffer, wherein ligands having increased affinity to the target relative to the first collected ligand mixture bind to the target; (f) removing unbound ligands; and (g) collecting the ligands that are bound to the target to produce a second collected ligand mixture to thereby identify ligands to the target. Even more preferably, ligands in the first or second collected ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the first collected ligand mixture with the target in the higher stringency buffer, after collecting the ligands that bound the target in the higher stringency buffer, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce a desired ligand.

In an alternative embodiment, the method comprises: (a) immobilizing a target on a substrate; (b) preparing a candidate mixture of potential ligands; (c) passing the candidate mixture over the substrate in a lower stringency buffer, wherein ligands having increased affinity to the immobilized target

relative to the candidate mixture bind to the immobilized target; (d) passing a wash buffer over the substrate to remove unbound candidate mixture; (e) passing an eluting buffer over the substrate to elute the ligands that are bound to the immobilized target to produce an eluted ligand mixture; (f) passing the eluted ligand mixture over a substrate comprising immobilized target in a higher stringency buffer, wherein ligands having increased affinity to the immobilized target relative to the eluted ligand mixture bind to the immobilized target; (g) passing a wash buffer over the substrate to remove unbound ligands; and (h) passing an eluting buffer over the substrate to elute the ligands that are bound to the immobilized target to thereby identify ligands to the target. With respect to the alternative embodiment, it also preferred that ligands in the eluted ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the eluted ligand mixture with the target in the higher stringency buffer, after eluting ligands that bound the target in the higher stringency buffer, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce as desired ligand. Thus, it is possible that the second collected ligand mixture can comprise a single ligand.

The method is applicable to any target as defined herein for which a ligand is sought. Representative targets are also disclosed in U.S. Patent Nos. 5,756,291 and 5,817,785 herein incorporated by reference. In a preferred embodiment, the method further comprises amplifying the eluted ligand to yield a ligand-enriched mixture, whereby a ligand to the target is identified. The ligand mixture can comprise a candidate mixture of any ligand as defined herein, including but not limited to nucleic acids. In this case, the candidate mixture of nucleic acids comprises single strand nucleic acids. The single stranded nucleic acids can comprise deoxyribonucleic acids.

Preferably, the single stranded nucleic acids are ribonucleic acids. In this case amplification can be accomplished, for example, via reverse transcriptase PCR reactions, as disclosed in U.S. Patent No. 5,817,785, herein incorporated by reference. Optionally, the candidate mixture of nucleic acids can comprise 2'-modified ribonucleic acids. For example, the 2'-modified ribonucleic acids can comprise 2'-fluoro (2'-F) modified nucleic acids.

Representative wash and eluting buffers are disclosed in U.S. Patent

Nos. 5,475,096 and 5,861,254, each of which incorporated herein by reference. In a preferred embodiment of the present invention in which a test nucleic acid mixture is incubated with target protein, the nucleic acid/protein mixture is filtered through a nitrocellulose filter and washed with appropriate buffer to remove free nucleic acids. Protein/nucleic acids often remain bound to the filter. Filter washing procedure can be optimized to reduce background binding. Such optimization of the filter washing procedures is within the skill of the ordinary artisan.

Any suitable eluting buffer as would be apparent to one of ordinary skill in the art after reviewing the disclosure of the present invention presented herein can also be employed in the present inventive method. For example, with respect to nucleic acid ligands, in order to proceed to the amplification step, selected nucleic acids must be released from the target after partitioning. This process is preferably done without chemical degradation of the selected nucleic acids and preferably results in amplifiable nucleic acids. For example, selected RNA molecules can be eluted from nitrocellulose filters using a freshly made solution containing 200 µl of a 7M urea, 20 mM sodium citrate (pH 5.0), 1 mM EDTA solution combined with 500 µl of phenol (equilibrated with 0.1M sodium acetate pH 5.2). A solution of 200 µl 7M urea with 500 µl of phenol can also be employed. In this case, the eluted solution of selected RNA can then extracted with ether, ethanol precipitated, and the precipitate re-suspended in water. A number of different buffer conditions for elution of selected RNA from the filters can be used. For example, without limitation non-detergent aqueous protein denaturing agents such as quanidinium chloride, quanidinium thiocyanate, etc., as are known in the art, can be used. The specific solution used for elution of nucleic acids from the filter can be routinely selected by one of ordinary skill in the art.

As is understood in the art, the concentration of various ions, in particular, the ionic strength, and the pH value impact on the value of the dissociation constant of the target/ligand complex. Thus, the terms "lower stringency" and "higher stringency" pertain to such buffer conditions (e.g. binding buffer conditions) as salt concentration, ionic strength generally, pH, temperature, or organic solvents, as will be readily appreciated by those skilled in the art after review of the disclosure presented herein.

The method can further comprise step (i): repeating steps (e), (f) and (g) (preferred embodiment) or repeating steps (f), (g) and (h) (alternative embodiment) in a higher stringency buffer. Optionally, the higher stringency buffer comprises a physiological buffer. As used herein, "physiological conditions" means the salt concentration and ionic strength in an aqueous solution that characterize fluids found in human metabolism commonly referred to as physiological buffer or physiological saline. In general, these are represented by an intracellular pH of 7.1 and salt concentrations (in mM) of Na^+: 3-15; K^+: 140; Mg^{+2}: 6.3; Ca^{+2}: 10-14 ; Cl^-:3-15, and an extracellular pH of 7.4 and salt concentrations (in mM) of Na^+:145; K^+:3; Mg^{+2}: 1-2; Ca^{+2}: 1-2; and Cl^-: 110. The use of physiological conditions in the ligand selection method is important, particularly with respect to those ligands that can be intended for therapeutic use.

V.A. Modified SELEX

Systematic Evolution of Ligands by EXponential Enrichment, SELEX, is essentially a powerful iterative affinity purification process that can be employed to isolate rare ligands from nucleic-acid combinatorial libraries. As such, it is necessary to establish conditions under which the desired activity (e.g., binding a coagulation factor, angiogenesis factor or E2F) can be detected in the initial randomized library prior to initiating the SELEX process. In addition, to purify ligands possessing this activity from other sequences within the randomized pool, the signal of the desired activity must be above the "noise" of library binding to the partitioning scheme (i.e., the fraction of sequences binding to the partitioning media due to target protein binding must be greater than those binding in a target independent manner).

Generally, the SELEX process can be defined by the following series of steps:

(1) A candidate mixture of nucleic acids of differing sequence is prepared. The candidate mixture generally includes regions of fixed sequences (i.e., each of the members of the candidate mixture contains the same sequences in the same location) and regions of randomized sequences. The fixed sequence regions are selected either: (a) to assist in the amplification steps described below; (b) to facilitate mimicry of a sequence

known to bind to the target; or (c) to enhance the concentration of a given structural arrangement of the nucleic acids in the candidate mixture. The randomized sequences can be totally randomized (i.e., the probability of finding a base at any position being one in four) or only partially randomized (e.g., the probability of finding a base at any location can be selected at any level between 0 and 100 percent).

(2) The candidate mixture is contacted with the selected target under conditions favorable for binding between the target and members of the candidate mixture. Under these circumstances, the interaction between the target and the nucleic acids of the candidate mixture can be considered as forming nucleic acid-target pairs between the target and the nucleic acids having the strongest affinity for the target.

(3) The nucleic acids with the highest affinity for the target are partitioned from those nucleic acids with lesser affinity to the target. Because only an extremely small number of sequences (and possibly only one molecule of nucleic acid) corresponding to the highest affinity nucleic acids exist in the candidate mixture, it is generally desirable to set the partitioning criteria so that a significant amount of the nucleic acids in the candidate mixture (approximately 5-50%) are retained during partitioning.

(4) Those nucleic acids selected during partitioning as having the relatively higher affinity to the target are then amplified to create a new candidate mixture that is enriched in nucleic acids having a relatively higher affinity for the target.

(5) By repeating the partitioning and amplifying steps above, the newly formed candidate mixture contains fewer and fewer unique sequences, and the average degree of affinity of the nucleic acids to the target will generally increase. Taken to its extreme, the SELEX process will yield a candidate mixture containing one or a small number of unique nucleic acids representing those nucleic acids from the original candidate mixture having the highest affinity to the target molecule.

The desired characteristics for a given nucleic acid ligand can vary. All nucleic acid ligands are capable of forming a complex with the target. In some cases, it is desired that the nucleic acid ligand will serve to inhibit one or more of the biological activities of the target. In other cases, it is desired that the

nucleic acid ligand serves to modify one or more of the biological activities of the target. In other cases, the nucleic acid ligand serves to identify the presence of the target, and its effect on the biological activity of the target is irrelevant.

5   In order to identify conditions that are preferred for the initiation of the SELEX process (i.e., signal to noise ratio >2) a matrix strategy to test for target dependent versus target independent binding of the library under different conditions is provided in accordance with the present invention. While this strategy is employed to identify SELEX conditions that are

10   physiologic or that approach physiologic for the target protein, it could readily be applied to identify very non-physiologic conditions if one desired to use an aptamer in downstream processes that require solvents that are non-physiologic.

    In one embodiment of the matrix, the monovalent salt concentration

15   and pH of the binding buffer are varied in combination to test monovalent salt concentrations from 10 (low stringency) to 150 mM (high stringency) and a pH range from 7.0-8.0 in binding reactions with radiolabeled randomized library RNA and varying concentrations of target protein. All binding buffers also contain physiologic concentrations of the appropriate divalent metal ions

20   (depends on the *in vivo* compartment of the target) and excipient as needed to maintain the protein in solution in a native state. This systematic variation of these critical parameters allows for the rapid identification of the buffer conditions and target concentration under which the SELEX process can be successfully initiated. In some cases, the initial conditions are non-

25   physiologic with respect to the monovalent salt concentration, the pH, or both. In these cases, the matrix strategy can be employed again in subsequent rounds of the SELEX process to determine when the conditions (i.e. binding buffer) of the SELEX can be changed. This strategy is repeated every few rounds until the SELEX process can be continued under physiologic

30   conditions.

V.B. Toggle Method

    Another embodiment of a method of identifying a ligand to a target from a candidate mixture of potential ligands is provided in accordance with the

present invention. Products, i.e., ligands, produced or identified via the method are also provided in accordance with the present invention.

The method preferably comprises: (a) providing a target selected from a first species of organism; (b) preparing a candidate mixture of potential ligands; (c) contacting the candidate mixture with the target, wherein ligands having increased affinity to the target from the first species of organism relative to the candidate mixture bind to the immobilized target from the first species of organism; (d) removing unbound candidate mixture; (e) collecting the ligands that are bound to the target from the first species of organism to produce a first collected ligand mixture for the target; (f) contacting the first collected ligand mixture with a target from a second species of organism, the target from the second species having at least a portion thereof that is substantially homologous to the same portion in the target from the first species, wherein ligands having increased affinity to the target from the second species relative to the first collected ligand mixture bind to the target; (g) removing unbound first collected ligand mixture; and (h) collecting the ligands that are bound to the target from the second species of organism to form a second collected ligand mixture thereby identify ligands to the target.

Preferably, ligands in the first or second collected ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the first collected ligand mixture with the target from the second species of organism, after collecting the ligands that bound the target from the second species of organism, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce a desired ligand. Thus, it is possible that the second collected ligand mixture can comprise a single ligand.

Another embodiment of a method of identifying a ligand to a target from a candidate mixture of potential ligands in accordance with the present invention comprises: (a) immobilizing a target on a substrate, the target comprising a target selected from a first species of organism; (b) preparing a candidate mixture of potential ligands; (c) passing the candidate mixture over the substrate, wherein ligands having increased affinity to the immobilized target from the first species of organism relative to the candidate mixture bind to the immobilized target from the first species of organism; (d) passing a

wash buffer over the substrate to remove unbound candidate mixtures; (e) passing an eluting buffer over the substrate to elute the ligands that are bound to the immobilized target from the first species of organism to produce an eluted ligand mixture; (f) passing the eluted ligand mixture over a substrate comprising an immobilized target from a second species of organism, the target from the second animal species contacting the first collected ligand mixture, the target from the second species having at least a portion thereof that is substantially homologous to the same portion in the target from the first species, wherein ligands having increased affinity to the target from the second species relative to the first collected ligand mixture bind to the immobilized target; (g) passing a wash buffer over the substrate to remove unbound eluted ligand mixture; and (h) passing an eluting buffer over the substrate to elute the ligands that are bound to the immobilized target from the second species of organism to thereby identify ligands to the target.

Preferably, ligands in the first or second collected ligand mixture are enriched or expanded by any suitable technique, e.g. amplification, prior to contacting the first collected ligand mixture with the target from the second species of organism, after collecting the ligands that bound the target from the second species of organism, or both. Optionally, the contacting and expanding or enriching steps are repeated as necessary to produce a desired ligand. Thus, it is possible that the second collected ligand mixture can comprise a single ligand.

Optionally, the method can further comprise further comprising step (i): repeating steps (f), (g) and (h) one or more times, wherein each additional time alternates between the target from the first species and the target from the second species. The method can also further comprise amplifying the eluted ligand to yield a ligand-enriched mixture, whereby a ligand to the target is identified.

The method is applicable to any target and to any ligand as defined herein for which a ligand is sought. Representative targets are also disclosed in U.S. Patent No. 5,756,291, herein incorporated by reference. Alternation of the target between homologous proteins of different species ensures that the products of selection will bind to both proteins, most likely to domains conserved between the two proteins. Because conserved domains tend to be

functionally important, driving the selection with homologous proteins can be advantageous even when species cross-reactivity is not necessarily sought. Similarly, the toggle approach is generalizable to homologous proteins of different viral strains and to related proteins of the same species (such as
5   receptor or ligand families with redundant or overlapping function), where cross-reactivity can improve *in vivo* efficacy. Thus, the phrase "the target from the second species having at least a portion thereof that is substantially homologous to the same portion in the target from the first species" includes but is not limited to conserved domains.

10   The term "substantially homologous" in the context of two or more polypeptide sequences is measured by polypeptide sequences having about 35%, or 45%, or preferably from 45-55%, or more preferably 55-65%, or most preferably 65% or greater amino acids which are identical or functionally equivalent. Percent "identity" and methods for determining identity are
15   defined herein below. Further, this term also encompasses proteins typically referred to in the art as homologues, e.g. porcine and human thrombin as disclosed in the Examples.

Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) *Adv Appl*
20   *Math* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J Mol Biol* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc Natl Acad Sci USA* 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group,
25   Madison, WI), or by visual inspection (<u>See</u> *generally,* Ausubel et al. (1992)).

A preferred algorithm for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. (1990) *J Mol Biol* 215: 403-410. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information
30   (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial

neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength W=11, an expectation E=10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix. See Henikoff and Henikoff (1989) *Proc Natl Acad Sci USA* 89:10915.

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) *Proc Natl Acad Sci USA* 90:5873-5887. One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

In a preferred embodiment, the method further comprises amplifying the eluted ligand to yield a ligand-enriched mixture, whereby a ligand to the target is identified. The ligand mixture can comprise a candidate mixture of nucleic acids. In this case, the candidate mixture of nucleic acids can comprise single strand nucleic acids. The single stranded nucleic acids can

comprise deoxyribonucleic acids.

Preferably, the single stranded nucleic acids are ribonucleic acids. In this case amplification can be accomplished, for example, via reverse transcriptase PCR reactions, as disclosed in U.S. Patent No. 5,817,785, herein incorporated by reference. Even more preferably, the candidate mixture of nucleic acids comprises 2'-modified ribonucleic acids. Even more preferably, the 2'-modified ribonucleic acids comprise 2'-fluoro (2'-F) modified nucleic acids.

Contemplated species of organism include plants, animals, bacteria, fungi, viruses or other organism. Preferred species of animals include warm-blooded vertebrates, including but not limited to humans, rats, mice, pigs, apes, monkeys, cats, dogs, cattle, oxen, sheep, goats and horses, or other mammal typically used in experiments. Additional species include domesticated fowl, i.e., poultry, such as turkeys, chickens, ducks, geese, guinea fowl, and the like, as they are also of economical importance to humans. Thus, the term "avian" as used herein refers to any avian species, including but not limited to Gallinacea sp., chicken, turkey, duck, goose, quail and pheasant. Chicken is currently preferred.

Fish represent a category of animals of interest for agricultural and ecological reasons. Representative fish species include, but are not limited to, trout, salmon, carp, shark, ray, flounder, sole, tilapia, medaka, goldfish, guppy, molly, platyfish, swordtail, zebrafish, loach, catfish, and the like. Representative general techniques that are applicable to fish have been described by Ozato et al, *Cell Differ.*, 19:237-244 (1986), Inoue et al, *Cell Differ. Dev.*, 29:123-128 (1990), Rokkones et al, *J. Comp. Physiol.* B, 158:751-758 (1989), and Guyomard et al, *Biochimie*, 71:857-863 (1989), describing preparation of transgenic medaka, medaka, salmon and trout, respectively.

Laboratory Examples

The following Laboratory Examples have been included to illustrate preferred modes of the invention. Certain aspects of the following Laboratory Examples are described in terms of techniques and procedures found or contemplated by the present inventors to work well in the practice of the

invention. These Laboratory Examples are exemplified through the use of standard laboratory practices of the inventors. In light of the present disclosure and the general level of skill in the art, those of skill will appreciate that the following examples are intended to be exemplary only and that numerous changes, modifications and alterations can be employed without departing from the spirit and scope of the invention.

Example 1

Initial condition matrix to coagulation factor VIIa

Referring now to Figure 8, radiolabeled 2'fluoropyrimidine-modified library RNA was incubated with varying concentrations of coagulation factor VIIa in 9 different buffers, and target-bound versus free RNA was determined using the double-filter nitrocellulose filter binding assay (Wong and Lohman, 1993, *Proc. Natl. Acad. Sci. USA* 90, 5428-5432). For all conditions, the binding buffers contain 20 mM Hepes at the pH shown, 2 mM $CaCl_2$, and NaCl at the concentration shown. From the left to right in each set of 4, the factor VIIa concentration is 5 µM, 1.67 µM, 0.56 µM and no target. The fraction of the pool that binds factor VIIa decreases dramatically as the monovalent salt increases, but is relatively unaffected by the change of pH at a given NaCl concentration. In addition, the fraction of RNA bound in the absence of target is much greater at lower NaCl concentrations and lower pH.

In this Example, there is essentially no target binding above background under physiologic conditions (pH 7.4, 150 mM NaCl). Thus, if the SELEX process were initiated under these conditions it would fail outright. Likewise, at pH 7.0, 50 mM NaCl, there is significant target dependent binding, but also significant target independent binding. Were the SELEX initiated under these conditions, it would also likely fail. Preferred initiating conditions are pH 7.4, 50 mM NaCl, with a relatively high (µM) concentration of factor VIIa.

Example 2

Initial Condition Matrix to Coagulation Factor IXa.

Referring now to Figure 9, radiolabeled 2'fluoropyrimidine-modified library RNA was incubated with varying concentrations of coagulation factor

IXa in 6 different buffers, and target-bound versus free RNA was determined using the double-filter nitrocellulose filter binding assay. For all conditions, the binding buffers contain 20 mM Hepes at the pH shown, 2 mM $CaCl_2$, and NaCl at the concentration shown. From left to right in sets of 6, the FIXa concentration decreases 2 fold at each point from 5 μM to 0.31 μM, and the sixth point is the no target control.

The fraction of the pool that binds factor IXa decreases dramatically as the NaCl concentration increases. In this Example, there is low but detectable binding of the pool to factor IXa under physiologic conditions, and the SELEX process could be successfully initiated under these conditions. However, a preferred initiating condition would be pH 7.4, 50 mM NaCl, followed by a change to physiologic buffer in the early rounds of the SELEX process.

Example 3

Toggle SELEX

Species cross-reactivity facilitates the pre-clinical evaluation of potentially therapeutic molecules in animal models. This Example describes an *in vitro* selection strategy in which RNA ligands (aptamers) that bind both human and porcine thrombin were selected by "toggling" the protein target between human and porcine thrombin during alternating rounds of selection. The "toggle" selection process yielded a family of aptamers, all of which bound both human and porcine thrombin with high affinity. TOGGLE-25, a characteristic member, inhibited two of thrombin's most important functions: plasma clot formation and platelet activation. If appropriate targets are available, the toggle strategy is a simple measure that promotes cross-reactivity and can be generalizable to related proteins of the same species as well as to other combinatorial library screening strategies. This strategy should facilitate the isolation of ligands with needed properties for gene therapy and other therapeutic and diagnostic applications.

Anti-thrombin therapeutics have been of great interest due to thrombin's central role in blood coagulation as well as to its suggested role in cellular proliferation (intimal hyperplasia) following vascular injury. To develop a method for the generation of aptamers that would be clinically useful in humans and testable in animal models, a novel selection strategy was applied

to this previously validated target. Nuclease-resistant RNA ligands that bind both human and porcine thrombin were selected by "toggling" the protein target between human and porcine thrombin during alternating rounds of selection (Figure 31). Such cross-reactive aptamers inhibit both porcine and

5 human thrombin activity as might be expected from ligands made to bind evolutionally conserved regions of a protein.

A library containing approximately 10^{14} different RNAs was screened for those molecules that bind both human and porcine thrombin. In the first round of *in vitro* selection, the starting library was incubated with both human

10 and porcine thrombin (F2). RNAs that bound either protein were recovered and amplified to generate a library enriched in F2-binding RNAs. In round 2 of selection, the enriched library of RNAs was incubated with human F2 alone, and bound RNAs were recovered and amplified to generate a library of RNAs that had been further enriched for members that bound surfaces on human F2

15 (Figure 31). In round 3, this human-focused library was incubated with porcine F2, and the subset of RNAs that bound the porcine protein were recovered and amplified to generate a library that had been further enriched for binding structural motifs that were conserved between the F2 homologs. This "toggle" selection process was repeated during rounds 4 – 13 of SELEX utilizing the

20 human protein for even rounds and the porcine protein for odd rounds. In parallel, thirteen (13) rounds of standard SELEX were performed against the individual human and porcine proteins. To determine if toggle SELEX enriched for aptamers that cross-reacted with both human and porcine F2, binding properties of the RNA pools from various rounds of selection were

25 evaluated .

Early in the selection (round 3), no significant differences in the binding affinities of RNA pools from the human, toggle, or porcine selections were observed for either human F2 (Figure 32A) or porcine F2 (Figure 32B). By round 11, however, RNA pools selected against human F2 alone had less

30 avid binding for porcine F2 (Figure 32C), and RNA pools selected against porcine F2 alone had less avid binding for human F2 (Figure 32D), suggesting the presence of species-specific ligands within these pools; whereas RNA pools generated via toggle SELEX bound both human and porcine F2 as well as did RNA pools generated against each protein alone (Figure 32C and

32D). With continued selection, the differential binding of porcine selection RNA pools for human F2 was diminished (Figure 32E), and the differential binding of the human selection RNA pools for porcine F2 was lost (Figure 32F), indicating the loss of species-specific ligands from these pools.

5   Three *in vitro* selections were performed in parallel: human thrombin, porcine thrombin, and a toggle selection using alternating rounds of human and porcine thrombin in a SELEX process as disclosed in Examples 1 and 2 above. After thirteen rounds of the SELEX process, the pools were cloned and sequenced. The random sequences of seven clones of high affinity for

10   one another are shown in Figure 11. Some of the sequences shown in Figure 11 were represented in more than one selection but are only listed once in Figure 11 for clarity.

Thus, the amplification products from round 13 of each selection were cloned and sequenced. Thirteen clones analyzed from the human selection

15   had identical sequences (HUMAN-1). Consistent with round 13 binding data (Figure 32E and 32F), HUMAN-1 RNA bound both human and porcine F2 with high affinity. Thus, the selection to human F2 appears to have been driven to completion and yielded an aptamer that binds an epitope present on both the human and porcine proteins. Sequences from earlier rounds, when

20   multiple aptamers were still present, were not analyzed. All sequences from the toggle selection and 10 of 14 sequences from the porcine selection shared a conserved motif with the predominant human selection sequence: ACAAAGCUGRAGWACUUA (SEQ ID NO:227), where R represents A or G and W represents A or U. RNAs possessing the consensus sequence shared

25   similarly high binding affinities for both human F2 (K_d's ranging from 1 to 4 nM) and porcine F2 (all K_d's < 1 nM). A representative RNA, TOGGLE-25, bound human F2 with a K_d of 2.8 ± 0.7 nM and bound porcine F2 with a K_d of 83 ± 3 pM. A unique RNA from the porcine selection (PIG-10) bound porcine F2 with a K_d of 50 ± 8 pM but bound human F2 with a K_d of greater than 600

30   nM, demonstrating greater than 10,000-fold specificity for porcine F2 over human F2. Thus, the porcine thrombin selection yielded two classes of high affinity ligands. One recognizes an epitope that is conserved on human F2 while the other recognizes an epitope that is not conserved. Interestingly, the two RNAs compete for binding to porcine F2, suggesting that they bind

overlapping regions of the protein. These two RNAs are further characterized below.

A fundamental problem in the development of new therapies is that potentially useful therapeutic agents might not progress from bench top to clinical trials due to lack of demonstrated efficacy in animal models. Drug discovery strategies generally employ human targets, and the inability to cross-react with homologous targets of other species can interfere with pre-clinical testing. This Example discloses a high-affinity inhibitor of the protease thrombin using a novel *in vitro* selection strategy. The "toggle" selection strategy exploits the malleability of iterative *in vitro* techniques and is generalizable to other combinatorial library screening strategies. Alternation of the target between homologous proteins of different species ensures that the products of selection will bind to both proteins, most likely to domains conserved between the two proteins. Because conserved domains tend to be functionally important, driving the selection with homologous proteins can be advantageous even when species cross-reactivity is not necessarily sought. Similarly, the toggle approach is generalizable to homologous proteins of different viral strains and to related proteins of the same species (such as receptor or ligand families with redundant or overlapping function), where cross-reactivity can improve *in vivo* efficacy.

For a relatively well-conserved protein like thrombin (85% amino acid homology between human and bovine thrombin (Butkowski, R. J., et al. (1977) *J. Biol. Chem.* 252:4942-4957), aptamers selected against human thrombin might cross-react with thrombin of other species. A single-stranded DNA aptamer to human thrombin inhibits thrombin function in canine and ovine models, although relative binding affinities have not been reported. DeAnda, A., Jr., *et al.* (1994) *Ann. Thorac. Surg.* 58:344-350; Griffin, L. C., et al. (1993) *Blood* 81:3271-3276. The single aptamer identified from round 13 of the selection against human thrombin happened to cross-react with porcine thrombin; however, aptamers from earlier rounds where species-specificity was observed were not analyzed, and these RNA pools likely included species-specific aptamers. The identification of a species-specific aptamer from the porcine selection underscores the point that—even for selection

against a well-conserved protein—species cross-reactivity should not be assumed.

The "toggle" selection yielded a family of aptamers, all of which bound both human and porcine thrombin with high affinity. Although selection against
5   both targets could theoretically sacrifice affinity for the human target, this "toggle" family demonstrated affinity for human thrombin similar to RNAs generated against human thrombin alone. Furthermore, the potential loss in binding affinity should be outweighed by the potential gain in activity expected from driving selection toward evolutionarily conserved regions of the protein.
10   TOGGLE-25, a characteristic member of the "toggle" family, inhibited two of thrombin's most important functions: plasma clot formation and platelet activation. Truncation of the full-length aptamer to approximately 40 nt or fewer is preferred for efficient chemical synthesis, but minimization can have varying effects on binding and inhibitory activity. A 25-nt truncate (TOGGLE-
15   25t) retained the inhibitory activities of the full-length aptamer and demonstrated greater potency, particularly in plasma-based assays. The superiority of the TOGGLE-25t truncate in these assays might be attributable to slightly higher affinity for thrombin as well as theoretically less nonspecific binding to positively-charged plasma proteins.

20   Thrombin aptamers can fulfill a clinical need for more and better anticoagulants and antithrombotics. Widely utilized agents such as heparin and platelet surface receptor antagonists are effective but are limited by bleeding complications due to Heparin Induced Thrombocytopenia and irreversibility, respectively. The plasma stability of our aptamer has been
25   increased by the substitution of endonuclease-resistant nucleotides, which typically confer an *in vitro* half-life of greater than 5 hours as compared to 30 to 60 minutes for DNA and seconds for unmodified RNA. Pieken, W. A., et al. (1991). *Science* 253:314-317; Beigelman, L., *et al.* (1995) *J. Biol. Chem.* 270:25702-25708. Due to its small size and stability in plasma, its *in vivo* half-
30   life is governed by the rate of renal clearance, which can be reduced by the addition of various inert high molecular weight or hydrophobic groups Willis, M. C., *et al.* (1998) (published erratum appears in *Bioconjug Chem* 1998 Sep-Oct;9(5):633) *Bioconjug. Chem.* 9:573-582; Tucker, C. E., *et al.* (1999). *Journal of Chromatography. B, Biomedical Sciences & Applications* 732:203-

212. Depending on the planned application, therefore, our aptamer can be modified to have an *in vivo* half-life of minutes or hours. In addition, the high affinity of the aptamer can be exploited to more effectively block the thrombogenic and mitogenic effects of thrombin on platelets, fibroblasts, endothelium, and smooth muscle, which are believed to be mediated by proteolytic activation of a novel family of receptors, Protease-Activated Receptors or PARs.

Aptamers are a promising class of molecules, for target validation as well as for diagnosis and therapy. Nuclease-resistant aptamers have already proven to be useful reagents for the study of extracellular targets in a variety of disease processes, and animal studies have paved the way for the first clinical trials of an aptamer against VEGF in the wet form of age-related macular degeneration. In addition, gene therapeutic methods utilizing viral constructs have been used to "express" unmodified RNA aptamers against intracellular targets. Sullenger, B. A., et al. (1990) *Cell* 63:601-608; Good, P. D., et al. (1997) *Gene Ther.* 4:45-54. Species cross-reactivity will greatly facilitate the transition of these molecules from *in vitro* assays to animal models to human subjects. If the appropriate targets are available, the toggle strategy is a simple measure that promotes cross-reactivity. Because the selection process is performed *in vitro*, possible schemes to manipulate the specificity of an aptamer for the targeted protein(s) are virtually unlimited.

Accordingly, the present invention provides a method to isolate the therapeutic compounds against human (or other species) molecular targets such that the therapeutic compound cross-reacts with homologous molecular targets from another species. For example, this process can entail the selection of a therapeutic compound against a human target molecule of interest followed by selection against a homologous molecule from another species. This process yields compounds that can be evaluated in a predetermined preclinical animal model by isolating molecules that cross-react with the species that is of interest.

As disclosed in this Example, an aptamer to human thrombin that cross reacts with human porcine thrombin has been produced using this method. Moreover, this toggle selection approach is expected to yield compounds that

interact with functionally conserved regions of the target molecule that are likely to be the functionally important regions on the target.

Example 4
Inhibition of the Activity of Coagulation Factor IXa

Referring now to Figure 2A, it was shown that RNA 9.3 (SEQ ID NO:3) inhibits the FIXa/FVIIIa catalyzed activation of FX. In Figure 2A, factor IXa (0.5 nM) was equilibrated with no RNA (▲), 10 nM control RNA (■), or 10 nM RNA 9.3 (●). The FX activation reaction was initiated by the addition of FVIIIa (1 nM), PC/PS vesicles (100 µM) and FX (200 nM). The amount of FXa formed over time at 37°C was measured.

Referring now to Figure 2B, it was shown that RNA 9.3 (SEQ ID NO:3) prolongs the clotting time of human plasma. The clotting time of normal human plasma was measured in an aPTT assay in the absence of RNA (striped bar), or in the presence of increasing concentrations of control RNA (solid bar) or RNA 9.3 (SEQ ID NO:3) (open bar). The clotting time is expressed as the mean ± sem for duplicate measurements.

Example 5
Truncated FIXa Aptamers

The primary sequence of the minimal FIXa aptamers 9.3^t and 9.20^t are set forth in Table 1 above. The apparent K_d for binding of the 9.3 truncate 9.3^t to FIXa ranges from about 1 to about 3 nM, and to FIX ranges from about six (6) to about ten (10) nM. The apparent K_d of the 9.20 truncate 9.20^t for FIXa is ~100-200 nM.

Referring now to Figures 3A-3C, 9.3^t prolongs the clotting time of pig plasma as well as clotting time *in vivo* in a dose dependent manner as determined by aPTT clotting assays, ACT assays, and PT assays. The dose response curve is consistent with substantially complete inactivation of FIX/FIXa activity.

Examples 6A and 6B

Systemic Anticoagulation Model In Swine

Examples 6A and 6B pertain to the evaluation of the ability of the truncated FIX/FIXa aptamer, RNA 9.3 truncated aptamer 9.3^t (SEQ ID NO:70), to systemically anti-coagulate small (2-4 kg) swine. The evaluation included three groups with 3 animals per group. The groups are vehicle control (20 mM Hepes, pH 7.4; 150 mM NaCl; 2 mM CaCl$_2$), about 0.5 mg/kg aptamer in vehicle, and about 1.0 mg/kg aptamer in vehicle.

The following procedures were performed for each animal. Under anesthesia, a venous catheter was placed in the femoral vein of the pig for sample injection, and an arterial catheter was placed in the femoral artery for serial withdrawal of blood samples. Prior to injection, and at times thereafter, blood samples were taken and processed. One portion of the sample (~0.4 mls) was used to measure, on site, an activated clotting time (ACT) to establish a baseline whole blood clot time for each animal

A second portion of the sample (~2.7 mls) was aliquoted into citrate-containing Vacutainer^{TM} tubes and processed to prepare plasma for coagulation assays (e.g. aPTT's). A third portion of sample (~2.5 mls) was aliquoted into EDTA-containing Vacutainer^{TM} tubes and processed to prepare plasma to be used in the measurement of the plasma aptamer concentration. In addition, CBC's were performed prior to injection and at the end of the study.

Example 6A

Change in clot times following injection of vehicle or FIX/FIXa aptamer

Referring now to Figure 3B, the change in the Activated Clotting Time (ACT) following treatment with aptamer was measured. The ACT increase is the ratio of the (pre-injection ACT/post injection ACT) for each time point, 1.0=no change (time 0=pre-injection). There is a clear dose-dependent increase in the ACT of the aptamer but not vehicle treated animals, with a peak at ~4 min post injection for the low dose, and 4-6 min post injection for the high dose. At the lower dose, the effect persists out to nearly 15 minutes

post injection, while at the higher dose the ACT is still elevated at the conclusion of the experiment. Data is presented as the mean ± sem.

Referring now to Figure 3C, the change in the Prothrombin Time (PT) and activated Partial Thromboplastin Time (aPTT) following treatment with aptamer was also measured. The increase in the PT or APTT is the ratio of the (pre-injection clot time/post injection clot time) for each time point, 1.0=no change (time 0=pre-injection). The PT is sensitive to inhibitors of coagulation factors II, V, VII, and X, but not to inhibitors of factors VIII or IX. The APTT is sensitive to inhibitors of factor IX/IXa. There is a clear dose-dependent increase in the aPTT of aptamer treated but not vehicle treated animals, with the peak increase occurring at the earliest time point taken (1 minute). In contrast, the PT is unaffected by vehicle or either dose of aptamer, demonstrating the functional specificity of the FIX/FIXa aptamer for its target versus other coagulation factors.

An important difference between the aPTT/PT assays and the ACT assay is that in the aPTT and PT assays, the plasma is pre-warmed (3-5 minutes) *ex vivo* prior to measuring the clotting time. Therefore, while the ACT likely reflects the dynamics of the drug action *in vivo* (plasma distribution, kinetics of target binding etc.), the aPTT likely reflects the total plasma concentration of the aptamer at a given time post-injection. In Figure 3C, data is presented as the mean ± sem.

Example 6B
Change in Clot Times Following Injection Of 0.5 mg/kg 5' Cholesterol-Modified FIX/FIXA Aptamer Versus Unmodified FIX/FIXa Aptamer

Referring now to Figures 5A and 5B, the change in the ACT following treatment with the cholesterol-modified aptamer was evaluated. The addition of cholesterol to an aptamer is expected to increase the plasma residence time of an aptamer following intravenous injection. The ACT increase is the ratio of the (pre-injection ACT/post injection ACT) for each time point, 1.0=no change (time 0=pre-injection). The duration of the increase in the ACT of the pig is clearly longer following injection of the cholesterol modified aptamer, RNA 9.3 truncated aptamer 9.3^{t-C} (SEQ ID NO:70)-C, versus RNA 9.3 truncated aptamer 9.3^{t} (SEQ ID NO:70). Following treatment with 9.3^{t}, the

effect persists out to between 15 to 20 minutes post injection, while following treatment with RNA 9.3 truncated aptamer 9.3$^{t\text{-}C}$ (SEQ ID NO:70)-C, the ACT is still elevated at the conclusion of the experiment (about 180 minutes). Data is presented in Figures 5A and 5B is the average of duplicate measurements at each time point.

Referring now to Figure 5C, the change in the PT and aPTT following treatment with cholesterol-modified aptamer is depicted. The increase in the PT or aPTT is the ratio of the (pre-injection clot time/post injection clot time) for each time point, 1.0=no change (time 0=pre-injection). The PT is sensitive to inhibitors of coagulation factors II, V, VII, and X, but not to inhibitors of factors VIII or IX. The aPTT is sensitive to inhibitors of factor IX/IXa. There is a clear dose-dependent increase in the aPTT of aptamer treated animals with the peak increase occurring at the earliest time point taken (1 minute); whereas the PT is unaffected by either aptamer (see also Figure 3C).

Continuing with Figure 5C, following treatment with RNA 9.3 truncated aptamer 9.3^{t} (SEQ ID NO:70), the effect persists out to between about 30 minutes post injection (see also Figure 3C), while following treatment with RNA 9.3 truncated aptamer 9.3$^{t\text{-}C}$ (SEQ ID NO:70)-C, the aPTT is still elevated at the conclusion of the experiment (about 180 minutes). In addition, although both aptamers give a similar initial aPTT increase, the increase in the aPTT of the pig following injection of RNA 9.3 truncated aptamer 9.3$^{t\text{-}C}$ (SEQ ID NO:70)-C is greater than that increase following treatment with RNA 9.3 truncated aptamer 9.3^{t} (SEQ ID NO:70). This indicates that the plasma concentration of RNA 9.3 truncated aptamer 9.3^{t} (SEQ ID NO:70)-C decreases more slowly than the plasma concentration of RNA 9.3 truncated aptamer 9.3^{t} (SEQ ID NO:70) following intravenous injection. Data is presented in Figure 5C is the average of duplicate measurements at each time point.

Example 7

Inhibition of the Activity of Coagulation Factor Xa

RNA 10.14 (SEQ ID NO:73) inhibits the FXa/FVa catalyzed activation of prothrombin. As shown in Figure 7A, factor Xa (0.5 nM) was equilibrated with no RNA (▲), 100 nM control RNA (■), or 100 nM RNA 10.14 (●), the

prothrombin activation reaction was initiated by the addition of FVa (1 nM), PC/PS vesicles (100 µM) and prothrombin (200 nM), and the amount of thrombin formed over time at 37°C was measured.

Referring now to Figure 7B, the clotting time of normal human plasma was measured in a PT assay in the absence of RNA (striped bar), or in the presence of increasing concentrations of control RNA (solid bar) or RNA 10.14 (open bar). The clotting time is expressed as the mean ± sem for duplicate measurements.

Example 8

Inhibition of Platelet Activation Using Thrombin RNA Aptamers

In this Example the ability of a thrombin RNA aptamer produced by the toggle SELEX method described in Example 3 to inhibit platelet activation was evaluated. Referring to Figs. 11 and 12, human platelets were isolated and activated by 1 nM human thrombin, in the presence of 30 nM toggle 25 (TOG 25, SEQ ID NO: 55) RNA aptamer or nitrocellulose-binding control RNA aptamer. The protease activated receptor-1 (PAR-1) peptide ligand, SFLLRN (SEQ ID NO: 72), was used as a positive control. As shown in Figure 12, the TOG 25 aptamer inhibited platelet activation to about 10%, which compared favorably to the platelet samples that included no activator.

Referring now to Figure 13, porcine platelets were isolated and activated by 2 nM porcine thrombin in the presence of the 20 nM TOG 25 RNA aptamer or nitrocellulose-binding control RNA aptamer. As shown in Figure 13, the TOG 25 aptamer was also able to inhibit pig thrombin in that the activation of the pig platelets was maintained at levels compared to that observed in samples where thrombin was not present.

Referring now to Figure 14, activated partial thromboplastin time (aPTT) assays were performed on human and pig plasma in the presence of increasing concentrations of the toggle 30 (TOG 30, SEQ ID NO: 56) RNA aptamer that was also prepared using the toggle SELEX method described in Example 3. As shown in Figure 14, comparable effects were observed in both human and pig plasma with the TOG 30 RNA aptamer. A control aptamer had no effect on aPTT at these concentrations.

The data presented in this Example and in Figs. 11-14 clearly indicate

that the toggle SELEX method disclosed herein to provide aptamers that exhibit selectivity for multiple species. The toggle SELEX method of the present invention thus provides a methodology wherein an aptamer that is selected for a test species as well as an ultimate species in which the

5   treatment is to be applied (e.g., pigs and humans) can be identified. This compatibility facilitates the identification of aptamers or other ligands that have activity in a test animal will also have activity in a subject that will ultimately be treated with the aptamer or other ligand.

10   <div align="center">

Example 9

Mutation Analysis of Antithrombin RNA Aptamer
</div>

A proposed secondary structure of a 25 mer truncate of TOG 25 (TOG 25 short, SEQ ID NO: 57), is shown in Figure 15. The nonmutated or "wild-type" truncate binds human thrombin with a K_d of approximately 1 nM.

15   Continuing with Figure 15, the binding affinity of various mutants designed to disrupt the proposed stem region, the BULGE region, and the LOOP sequences are shown and are summarized as follows. In the NO STEM mutant, wherein cytosines are mutated to guanidine, the binding affinity is approximately 1 micromolar. In the BULGEUs region, uracil moieties are

20   mutated to adenine and the resulting dissociation constant is much greater than 1 nM. These mutations thus substantially impair the binding affinity of the TOG 25 short aptamer to thrombin. In the LOOPU1 mutation, uracil to adenine, produces an aptamer having a dissociation constant of about 250 nM. The LOOPU2 mutation, also uracil to adenine, produces an aptamer

25   having a dissociation constant of about 1 nM. Thus, the mutations in the STEM and BULGE regions have greater impact than those in the LOOP regions.

Referring now to Figure 16, the ability of the full-length TOG 25 RNA aptamer, the TOG 25 short RNA aptamer, and the BULGEUs RNA aptamer to

30   inhibit platelet activation is analyzed. Human platelets were isolated and activated by 1 nM human thrombin, in the presence of increasing combination of full length TOG 25 (TOG 25 FL, SEQ ID NO: 55), truncated TOG 25 (TOG 25 short, SEQ ID NO: 57), or a non-binding human truncate (BULGEUs, SEQ ID NO: 59). Both the TOG 25 FL and TOG 25 short aptamers substantially

inihibit platelet activation, with observed levels of platelet activation below 20%. In contrast, the mutant BULGEUs aptamer did not demonstrate an ability to inhibit platelet activation, with activation levels of approximately 90%. These data thus provide guidance to the design and selection of aptamers that provide the desired modulator effects.

Example 10

Inhibition of the Activity of Coagulation Factor VIIa

Referring now to Figs. 19A-19B, a factor VIIa aptamer RNA 16.3 (SEQ ID NO: 41) inhibits the activity of coagulation factor VIIa. RNA 16.3 inhibits the VIIa/TF catalyzed activation of FX. Factors VIIa and X were equilibrated with no RNA (□), 1 mM mutated non-binding RNA 16.3 m4 (■) as a composition control, or 1 μM RNA 16.3 (▲), and the FX activation was initiated by the addition of lapidated tissue factor. The amount of FXa formed over time at 25°C was measured. The amount of FXa formed over time is expressed as the mean ± sem for three or more experiments.

In Figure 19B, it is shown that RNA 16.3 prolongs the tissue factor induced clotting time of human plasma. The clotting time of human plasma was measured in a PT assay in the absence of RNA (striped bar), wherein the presence of varying concentrations of RNA 16.3 mutated non-binding M4 (solid bar) or 16.3 (open bar). The clotting time is expressed as the mean ± sem for duplicate experiments.

Example 11

Inhibition of the Activity of Coagulation Factor VIIa

A nuclease-resistant 2'amino pyrimidine-modified RNA aptamer that can block tissue factor/FVIIa catalyzed FX activation, and that can prolong the clotting time of human plasma are disclosed herein above in Section II.B., in Figure 10, and in Example 10. While a potent antagonist at room temperature, it was discovered that this antagonist is much less potent at physiologic temperature (likely due to the reduced stability of duplexes containing the 2'amino modification). Therefore, this Example pertains to the generations of additional FVIIa antagonists by performing SELEX using a

2'fluoropyrimidine-modified RNA library at 37°C (this modification yields duplexes with enhanced stability compared to standard RNA). Eleven (11) rounds of the SELEX experiment were completed.

Following completion of 11 rounds of SELEX against FVIIa, cDNAs
5 from the rounds 10 and 11 pools were cloned and sequenced. Representative sequences are set forth in Table 4 above. The round 11 pool binds FVIIa with a K_D of ~10 nM under physiologic conditions, which represents a >1000 fold enrichment in binding activity for FVIIa over the course of the SELEX process.

10 The highest affinity aptamers, sequences 10.15 (SEQ ID NO:75) and 11.12 (SEQ ID NO:88), both bind FVIIa tightly, with apparent K_d's of ~5-8 nM under physiologic conditions (Figure 23A). Both aptamers bind the zymogen FVII with similar affinity. Aptamers 10.15 and 11.12 are both potent anticoagulants of human plasma in vitro as demonstrated by their ability to
15 prolong Prothrombin Time (PT) clotting assays (Figure 23B). The *in vitro* anticoagulant activity of both aptamers is comparable to the anticoagulant activity of the most potent FVIIa antagonists currently available in the art. In addition, neither aptamer prolongs the clotting time of human plasma in Activated Partial Thromboplastin Time (APTT) clotting assays, as expected
20 for specific FVIIa antagonists. Generating active truncates of both of these aptamers allows production of these aptamers by chemical synthesis for *in vivo* analysis.

Example 12
Inhibition of the Activity of Coagulation Factor Xa
25 This Example pertains to the isolation of active truncates of aptamers generated against coagulation factor Xa (FXa). Shown in Figure 21 is the predicted secondary structure of a fully active 36 nucleotide version of aptamer 11.F7 (SEQ ID NO:148), a sequence related to the aptamer 10.14
30 (SEQ ID NO:73) described above. This aptamer, termed 11.F7[t], binds FXa with an apparent K_d of ~1.5 nM, and exhibits at least several hundred fold specificity for FXa versus related coagulation factors VIIa, IXa, XIa, APC and thrombin. This truncate is a potent anticoagulant of human plasma *in vitro* as demonstrated by its ability to prolong both the PT (Figure 22A) and APTT

(Figure 22B) clotting times. Based upon comparison to the *in vitro* anticoagulant activity of other FXa inhibitors described in the art, this aptamer is one of most potent FXa antagonists described. The activity of this aptamer in animal models of systemic anticoagulation and thrombosis is also provided, in accordance with the *in vivo* experiments disclosed in previous Examples.

Example 13
Modulation of the Activity of Ang1

This Example pertains to an analysis of the modulation of Ang1 by Ang1 RNA aptamers. To determine whether ANG9-4 (SEQ ID NO:151) binding inhibited Ang1 activity, 293 cells expressing human Tie2 were incubated with 13 nM Ang1* with or without a molar excess of 9-4 or control aptamer. ANG9-4 completely abrogated Tie2 autophosphorylation as detected by Western blotting with an antibody specific for phospho-Tie2 (pTie2)(see Figure 25).

As shown in Figure 26, cultured human endothelial cells were serum-starved and treated with TNFα (50 ng/ml) for 3 hours while being incubated with 3.5 nM Ang1* and either ANG9-4 or control aptamer. Apoptosis (DNA fragmentation) was measured by Cell Death Detection ELISA kit (Roche Molecular Biochemicals). ANG9-4, but not control aptamer, increased apoptosis in a dose-dependent manner. Neither 9-4 nor control RNA increased apoptosis in un-starved, un-treated cells.

Example 14
Modulation of the Activity of Ang2

As shown in Figure 28, cultured human endothelial cells were serum-starved and treated with TNFα (50 ng/ml) for 3 hours while being incubated with 15 nM Ang2 and either ANG11-1 or control aptamer. Apoptosis (DNA fragmentation) was measured by Cell Death Detection ELISA kit (Roche Molecular Biochemicals). ANG11-1, but not control aptamer, increased apoptosis to a levels above those seen in the absence of exogenous Ang2, suggesting inhibition of both exogenous and endogenous (autocrine) Ang2, which is known to be released by endothelial cells. Neither ANG11-1 nor control RNA increased apoptosis in non-irradiated cells.

As in Figure 29, the ability of ANG11-1 (SEQ ID NO:168) and a 41-nucleotide truncate (ANG11-1.41) (SEQ ID NO:189) to compete for binding to ANG2 (normalized to binding in the absence of competitor) is plotted as a function of competitor concentration. ANG11-1.41 competes for ANG2 binding with an affinity (K_d ~ 5 nM) only slightly worse that of the full-length RNA aptamer (~ 1 nM).

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The references listed below as well as all references cited in the specification are incorporated herein by reference to the extent that they supplement, explain, provide a background for or teach methodology, techniques and/or compositions employed herein.

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U.S. Patent No. 6,011,020

PCT Application WO 9203568

It will be understood that various details of the invention can be changed without departing from the scope of the invention. Furthermore, the foregoing description is for the purpose of illustration only, and not for the purpose of limitation--the invention being defined by the claims.

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